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    GenCore version
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ALIGNMENTS

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modulating Tie-2 tyrosine kinase activity, useful e.g. not growth, using vascular-endothelial protein tyrosine Protein tyrosine phosphatase, HPTP-beta, human, Tie-2; receptor-type tyrosine kinase, antiangiogenic, antitumour; antimetastatic; tumour; metastasis, angiogenesis; therapy. (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN Location/Qualifiers 1622. .1641 /note= "transmembrane domain" 1722. .1967 Human protein tyrosine phosphatase HPTP-beta. "catalytic domain" Disclosure; Page 21-27; 60pp; English AAB19774 standard; protein; 1997 AA ä Deutsch 99EP-00108074. 99EP-00108074 (first entry tumor growth, /note= 'n Risau WPI; 2000-648932/63 N-PSDB; AAA88966. Fachinger G, 23-APR-1999;. 23-APR-1999; sapiens EP1046715-A1 phosphatase. 19-FEB-2001 25-OCT-2000 Monitoring cregulating t AAB19774; Domain Domain Homo RESULT 1 Key AAB19774

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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Result Š. The present sequence is that of human protein tyrosine phosphatase HPTP-beta, a member of subclass III receptor type PTPs, bearing fibronectin type III-like repeats in the extracellular domain and a single catalytic domain in the cytoplasmic tail. HPTP-beta is a vascular-endothelial

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protein tyrosine phosphatase (VE-PTP) that specifically interacts with receptor-type tyrosine kinase Tie-2, modulating its tyrosine phosphorylation. Tie-2 is involved in angiogenetic processes, the formation of blood vessels during embryonal development, wound healing and in pathological processes such as tumour development. WE-PTPs such as HPTP-beta or its catalytic domain, nucleic acids and ligands can be used to monitor, stimulate or repress Tie-2 activity for the purpose of monitoring or modulating angiogenesis, inducing or inhibiting vascular growth or medelling and blood vessel maturation, and inhibiting tumour growth or metastasis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of compound useful for treatment of angiogenesis mediated disorder, by using three-dimensional structure of HPTPbeta catalytic domain, and employing structure to design, or select compound that binds HPTPbeta in silico.
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Human; lung specific gene; LSG; lung embryonic development; cytostatic; lung cancer; vaccine; gene therapy; non-cancerous lung disease; tumour.

1885. 1898 /note= "Antigenic epitope" 1967. 1974 145. .155 /note= "Antigenic epitope" "Antigenic epitope" epitope" 1281. .1295 'note= "Antigenic epitope" epitope" .644. .1655 'note= "Antigenic epitope" 1725. .1738 /note= "Antigenic epitope" 1748. .1759 "Antigenic epitope" "Antigenic epitope' "Antigenic epitope' "Antigenic epitope" "Antigenic epitope" 'note= "Antigenic epitope' "Antigenic epitope' /note= "Antigenic ep 1376. .1408 /note= "Antigenic ep 1532. .1545 Location/Qualifiers "Antigenic note= "Antigenic note= "Antigenic "Antigenic "Antigenic 307. .1318 1351. .1369 . 735 .465 .823 1804. .18 /note= "7 1532. .1 /note= ", note= 'note= 'note= /note= 'note= 'note= /note= 1334. Region Řey

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21-JUL-2000; 2000US-0219834P

(DIAD-) DIADEXUS INC

Chen S; Nair M, Macina RA,

WPI; 2002-268964/31.

Novel lung specific gene useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous disease states in lung, for gene therapy, and for identifying lung tissue.

Claim 2; Page 185-192; 197pp; English.

The present invention relates to lung specific genes (LSG) and their corresponding polypeptides. LSG is useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous disease states in lung, identifying lung tissue, monitoring and modifying lung embryonic development and differentiation, in gene therapy, as hybridisation probes, to detect LSG mRNA as a marker for lung cancer, as research reagents and materials for discovery of treatments and disease, to detect complementary polynucleotides, and for chromosome identification. An antibody which binds LSG is useful

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to detect or image localisation of LSG in a patient for detecting or diagnosing a disease or condition, for preventing the onset and treatmen of lung cancer, to isolate or to identify clones expressing LSG polypeptides, and to target tumours expressing LSG. The present sequence is human LSG protein Sequence 1997 AA;	Query Match Best Local Similarity 99.8%; Pred. No. 0; Matches 1993; Conservative 2; Mismatches 2; Indels 0; Gaps	1 MLSHGAGLALWITLSLLQTGLAEPERCNFTLAESKASSHSVSIQWRILGSPCNFSLIYSS 60	61 DTLGAALCPTFRIDNTTYGCNLQDLQAGTIYNFKIISLDBERTVVLQTDPLPPARFGVSK 120	121 EKTISTGLHVWWTPSSGKVTSYEVQLFDENNQKIQGVQIQESTSWNEYTFFNLTAGSKYN 180 	181 IAITAVSGGKRSFSVYTNGSTVFSPVKDIGISTKANSLLISWSHGSGNVERYRLMLMDKG 240	241 ILVHGGVVDKHATSYAFHGLSPGYLYNLTVMTEAAGLQNYRWKLVRTAPMEVSNLKVTND 300 241 ILVHGGVVDKHATSYAFHGLSPGYLYNLTVMTEAAGLQNYRWKLVRTAPMEVSNLKVTND 300	301 GSLTSLKVKWQRPPGNVDSYNITLSHKGTIKESRVLAPWITETHFKELVPGRLYQVTVSC 360 	361 VSGELSAQKMAVGRTFPDKVANLEANNNGRMRSLVVSWSPPAGDWEQYRILLFNDSVVLL 420	421 NITVGKEETQYVMDDTGLVPGRQYEVEVIVESGNLKNSERCQGRTVPLAVLQLRVKHANE 480	481 TSLSIMWQTPVAEWEKYIISLADRDLLLIHKSLSKDAKEFTFTDLVPGRKYMATVTSISG 540	541 DLKASSSYKGRTVPAQVTDLHVANQGMTSSLFTNWTQAQGDVEFYQVLLIHENVVIKNES 600	601 ISSETSRYSFHSLKSGSLYSVVVTTVSGGISSRQVVVEGRTVPSSVSGVTVNNSGRNDYL 660	661 SVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTITTRSGKYE 720	721	781 SENECVFVQLVPGRLYSVTVTTKSGQYEANEQGNGRTIPEPVKDLTLRNRSTEDLHVTWS 840	841 GANGDVDQYEIQLLFNDMKVFPFFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAF	941
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Tec; protein tyrosine kinase; protein tyrosine phosphatase; PTP10D; egg derived tyrosine phosphatase; EDTP; antidiabetic; hypotensive; cardiant; antilipaemic; osteopathic; cytostatic; ancretic; obesity; immunomodulator; gene therapy; metabolic disease; eating disorder; body weight regulation disorder; cachexia; diabetes mellitus; cancer; hypercheshon; coronary heart disease, hypercholsterolaemia; gallstone; dyslipidaemia; osteoarthritis; sleep apnea; human; chromosome 12; protein tyrosine phosphatase receptor type B precursor; PTPRB.
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                                                 ABR57179 standard; protein; 1997
                                                                                                           Human PTPRB protein SEQ ID NO:4.
1981 YENVNPEYHRDPVYSRH 1997
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07-DEC-2001; 2001EP-00129138.
02-JAN-2002; 2002EP-00000010.
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The present invention describes a pharmaceutical composition comprising a nucleic acid (1) protein tyrosine phosphatase PTP10D, non-receptor concleic acid (1) protein tyrosine phosphatase PTP10D, non-receptor composition kinase Tec. egg derived tyrosine phosphatase (BDTP) gene family or encoded polypeptide, fragment or variant of nucleic acid molecule of PTP10D, Tec. or BDTP gene family or encoded composition can have antidiabetic, hypotensive, cardiant, antilipaemic, composition can have antidiabetic, hypotensive, cardiant, antilipaemic, composition can have antidiabetic, hypotensive, cardiant, antilipaemic, or steopathic, cytostatic, anorectic and immunomodulator activities, and can be used in gene therapy. The composition is useful for the antidiation of an agent for detecting and/or varifying, for treating and can a number of an agent for detecting and/or varifying, for treating and alleviating and/or preventing a disorder, including metabolic diseases such as obesity and other body weight regulation disorders, as well as the and other body weight regulation disorders, as well as calleviating and other body weight regulation disorders, as well as calleviating and other body weight regulation disorders, as well as calleviation of seconary heart disease, hypercholesterolaemia, dysolutive organ), sleep apnea, and other diseases, in cells, cell masses, organs and/or subjects. The components of the composition may also be used in controlling the function of a spene and/or gene product which is influenced and/or modified by a PTP10D, Tec, or EDTP family or their fragments, may be used in the PTP10D, Tec, or EDTP family or their fragments, may be used in the composition of a non-human animal which over- or under-expresses the compositions comprising tyrosine phosphatase PTP10D, protein tyrosine use Tec or egg-derived tyrosine phosphatase genes or proteins, useful treating or preventing metabolic diseases, e.g. as obesity or Claim 2; Fig 8B; 83pp; English. cachexia kinase

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PTP10D, Tec, or EDTP gene product. The present sequence represents human protein tyrosine phosphatase receptor type B precursor (PTPRB), which is a human PTP10B homologous sequence. Human PTPRB is located to chromosome
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IEGFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVFE
                                   GVAERYDILLLTENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQTE
                                                                                  GVAERYDILLLTENGILLRNTSEPATTKOHKFEDLTPGKKYKIOILTVSGGLFSKEAQTE
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                           Huntington's disease; ostecarthritis;
Leber's hereditary optic neuropathy; LHON;
antochondrial encephalogathy lactic acidosis and stroke; MELAS;
mycolonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; noctropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
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20-SEP-2002; 2002US-0412418P.
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GSLTSLKVKWQRPPGNVDSYNITLSHKGTIKESRVLAPWITETHFKELVPGRLYQVTVSC 360
                                                                                       VSGELSAQKMAVGRTFPDKVANLEANNNGRMRSLVVSWSPPRAGDWEQYRILLFNDSVVLL
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                                                                                                                                         NITVGKEETQYVMDDTGLVPGRQYEVEVIVESGNLKNSERCQGRTVPLAVLQLRVKHANE
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in diagnosis and gene therapy.
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Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Yang Y, Wejhrman T, Goodrich R;
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   arthritis; inflammation.
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larity 99.8%; Pred. No. 0;
Conservative 1; Mismatches
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20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-006635135.
30-NOV-2000; 2000US-00693325.
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   disorder;
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N-PSDB; AAKS1954.
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Ma Y, Zh
Xue AJ,
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                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
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J, Ren F,
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Pred. No. 0;
1; Mismatches
                                                                                          Asundi V, Z
J, Zhang J,
Goodrich R;
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                                                                                            Drmanac RT,
Wang D, Wang
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Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
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Best Local Similarity 99.7%;
Matches 1992; Conservative 1
   20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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                                                        (HYSE-) HYSEQ INC
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Zhao C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a polypeptide comprising vascular endothelial-protein tyrosine phosphatase (WE-PTP) or its active fragment or effector, or the nucleic acid encoding the polypeptide or its effector, for use in the manufacture of an agent for monitoring or modulating VE-cadherin mediated processes or disorders. The polypeptide comprising vascular endothelial-protein-tyrosine phosphatase (WE-PTP) or its active fragment or effector, or the nucleic acid encoding the polypeptide or its effector, is useful for the manufacture of an agent for monitoring or modulating VE-cadherin mediated processes or disorders,
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gene therapy; cytostatic; VE-cadherin; vascular endothelial-cadherin.
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e.g., cancer. The present sequence is a protein shown in the exemplification of the invention Sequence 1998 AA;	λο qα .	
Query Match 87.0%; Score 9117.5; DB 7; Length 1998; Best Local Similarity 65.7%; Pred. No. 0; Matches 1713; Conservative 129; Mismatches 155; Indels 1; Gaps 1;	& g	
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17	λό q	1200 DFDFYELILYNPNGTKKENWKDK
23	ç Q	1260 APSPPSLMSFADIANTSLAITWR
GILVHGGVVDKHATSYAFHGLSPGYLYNLTVMTBAAGLQNYRWKLVRTAPMEVSNLKVTN 299 :	<i>&</i> 원	1320 YGLRPGKSYQFNVKTVSGDSWKT
ო ო	& 8 8	1380 SDFDGYSIECRKMDTQEVEFSRK
4 4	& A	1440 STITMIDRPPPPPPHIRVNEKOV
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ETSLSIMMQTPVAEWEKYIISLADRDLLLIHKSLSKDAKEFTFTDLVPGRKYMATVTSIS 539 - -	ර් සි	
GDLKASSSVKGRIVPAQVIDLHVANQGMISSLFINWIQAQGDVEFYQVLLIHENVVIKNE 599 	රු සි	
SISSETSRYSFHSLKSGSLYSVVVTTVSGGISSRQVVVEGRTVPSSVSGVTVNNSGRNDY 659	රු අ	
660 LSVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTITTRSGKY 719 	රු අ <u>අ</u>	
720 ENHSFSQERTVPDKVQGVSVSNSARSDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIP 779 	ଧ ଶ	1800 MYTCCVEKGRYKCDHYWPADODS
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SGANGDVDQYEIQLLFNDMKVFPPFHLVNTATEYRFTSLTBGRQYKILVLTISGDVQQSA 899 	. B &	20 ILQQLDSKDSVDIYGAVHL
FIEGFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVF 959 	∂ 8	1980 IYENVNPETHENPYVSKH 1997 1 1981 IYENVNPEYHRDAIYSKH 1998

1139 1140 1199 1200 WKGPPDWTDYNDFELQWLPRDALTVFNPYNRKSEGRIV 1319 KTYSKPIFGSVRTKPDKIQNLHCRPQNSTAIACSWIPPD 1379 KKLEKEKSLLNIMMLVPHKRYLVSIKVQSAGMTSEVVED 1439 VVLISKSSINFTVNCSWPSDTNGAVKYFTVVVREADGSD 1499 RAFTOLFDEDLKEFTKPLYSDTFFSLPITTESEPLFGA 1619 1679 1680 (LLSKEYEELKDVGRNQSCDIALLPENRCKNRYNNILPY 1739 SYIPGNNPRREYIVTQGDLPGTKDDFWKMYWEQNYHNIV 1799 1859 1919 1979 RVYQTNYFASKCAENPNSNSKSFNIKLGAEMESLGGKR 1559 SELKNOINVVGRTVPASVQGVIADNAYSSYSLIVSWQKA SFRWTASEGELSWYNIFLYNPDGNLQERAQVDPLVQSF SLYYGDLILOMLSESVLPEWTIREFKICGEEQLDAHRL CROKVSHGRERPSARLSIRRDRPLSVHLNLGOKGNRKT **QFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDR** HRVHMVQTECQYVYLHQCVRDVLRARKLRSEQENPLFP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a pharmaceutical composition comprising a nucleic acid (I) protein tyrosine phosphatase PTP10D, non-receptor nucleic acid (I) protein tyrosine phosphatase PTP10D, non-receptor family or encoded polypeptide, frament or variant of mucleic acid molecule of PTP10D, Tec. or EDTP gene family or encoded polypeptide, an antibody, an aptamer or receptor recognising composition can have antidiabetic, hypotensive, cardiant, antilipaemic, polypeptide, and a carrier, diluent and/or adjuvant. The pharmaceutical composition can have antidiabetic, hypotensive, cardiant, antilipaemic, osteopathic, cytostatic, anorectic and immunomodulator activities, and can be used in gene therapy. The composition is useful for the manufacture of an agent for detecting and/or verifying, for treating and can preventing a disorder, including metabolic diseases and alleviating and/or preventing a disorder, including metabolic diseases cuch as obesity and other body weight regulation disorders, as well as trelated disorders such as eating disorder, cachexia, diabetes mellitus, hypertension, coronary heart disease, hypercholesterolemia, crelated disorders such as eating disorder, cachexia, diabetes mellitus, hypertension, coronary heart disease, hypercholesterolemia, crelated disorders such as obsitive and other body weight regulation disorders, as well as caproductive organ), sleep apnea, and other diseases, in cells, cell masses, organs and/or subjects. The components of the composition may calso be used in controlling the function of a perplob, Tec, or EDTP family or their fragments, may be used in the present and protein tyrosine phosphatase receptor type B precursor (PTPRB) chamin and animal which over or under-expresses the companion acid sequence, which is given in comment in comparison with brosphila FTPRB is located in the exemplification of the present invention. Human PTPRB is located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New compositions comprising tyrosine phosphatase PTP10D, protein tyrosine kinase Tec or egg-derived tyrosine phosphatase genes or proteins, useful for treating or preventing metabolic diseases, e.g. as obesity or
                                                                                                                                                                            Tec; protein tyrosine kinase; protein tyrosine phosphatase; PTP10D; egg derived tyrosine phosphatase; BDTP; antidiabetic; hypotensive; cardiant; antilipaemic; osteopathic; cytostatic; anorectic; obesity; immunomodulator; gene therapy; metabolic disease; eating disorder; body weight regulation disorder; cachexia; diabetes mellitus; cancer; hyperrension; ocronary heart disease; hypercholssterolaemia; gallstone; dyslipidaemia; osteoarthritis; sleep apnea; human; chromosome 12; protein tyrosine phosphatase receptor type B precursor; PTPRB.
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                                    ABR57182 standard; protein; 1450 AA
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02-JAN-2002; 2002EP-00000010.
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Matches 1448; Conservative
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This invention relates to novel, isolated full length human cDNA clones and the encoded proteins thereof. Specifically, it refers to cDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as articolates, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these continuations of the CDNA molecules are useful for diagnostic markers or therapeutic targets for molecules are useful for diagnostic markers or therapeutic targets for the various disease, or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein cencede by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVTSYEVQLFDENNQKI QGVQI QESTSWNEYTFFNLTAGSKYNIAITAVSGGKRSFSVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 6712; DB; Pred. No. 0; 4; Mismatches
      Alzheimer's diseases, Parkinson's diseases,
                                     SEQ ID NO 3752; 2686pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6%;
Matches 1288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1407 AA;
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IRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKEYEELKDVGRNQS 1718
                                                                                                                                                                                                      LPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVL 1838
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                                                   SNSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKP
                                                                         SNSKSFNIKLGAEMESLGGKCDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKP
                                                                                                                  LYSDTFFSLPITTESEPLFGAIEGVSAGLFLIGMLVAVVALLICRQKVSHGRERPSARLS
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Nagai K,
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Wakamatsu A, Ishii S,
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                                                                                                                                                      VIVITKSGQYEANEQGNGRIIPEPVKDLILRNRSTEDLHVIWSGANGDVDQYEIQLLFND 954
                                                                                                                                                                                               MKVFPFFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEGFTVPSAVKNIHISP 917
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                                                                        SVSNSARSDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIPKSENECVFVQLVPGRLYS 797
                                                                                                                                   VTVTTKSGQYEANEQGNGRTIPEPVKDLTLRNRSTEDLHVTWSGANGDVDQYEIQLLFND 857
                               LSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTITTRSGKYENHSFSQRRTVPDKVQGV
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               LSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTITTRSGKYENHSFSQERTVPDKVQGV
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mouse; Tie-2; 24 'note= "membrane proximal fibronectin II domain" Vascular-endothelial protein tyrosine phosphatase; VE-PTP; receptor-type tyrosine kinase; antiangiogenic; antitumour; antimetastatic; tumour; metastasis; angiogenesis; therapy. Mouse vascular-endothelial protein tyrosine phosphatase Location/Qualifiers AAB19773 standard; protein; 579 Mus musculus AAB19773 Key Domain AAB19773 BXBXHLHHHHXSXKKKKKKKKKK 셤

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204. .223 /note= "transmembrane domain" 304. .549 /note= "catalytic domain"

Domain

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PEWTIREFKICGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAG

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LPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVL 1838 361 LPGTKDDFWKMAWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDPLYYGDLILQMVSESVL 420 The present sequence is that of murine vascular-endothelial protein tyrosine phosphatase (WE-PTP). WE-PTP is a member of subclass III receptor type PTPs, bearing fibronectin type III-like repeats in the extracellular domain and a single catalytic domain in the cytoplasmic tail. WE-PTP specifically interacts with receptor-type tyrosine kinase Tie-2, modulating its tyrosine phosphorylation. Tie-2 is involved in andiogenetic processes, the formation of blood vessels during embryonal development, wound healing and in pathological processes such as tumour development. WE-PTP or its catalytic domain, nucleic acids and ligands can be used to monitor, stimulate or repress Tie-2 activity for the purpose of monitor, stimulate or repress Tie-2 activity for the purpose of monitoring or modulating angiogenesis, inducing or inhibiting vascular growth or remodelling and blood vessel maturation, and inhibiting tumour growth and metastasis | SSSKSFNIKLGAEMDSLGGKCDPSQQKFCDGPLLPHTAYRLSIRAFTQLFDEDLKEFTKP 241 IRRDRPLSVHLNLGQKGNRKTSCPIKINQFBGHFWKLQADSNYLLSKBYEDLKDVGRSQS LYSDTFFSLPITTESEPLFGAIBGVSAGLFLIGMLVAVVALLICRQKVSHGRERPSARLS 181 LYSDTFFSMPITTESEPLFGVIEGVSAGLFLIGMLVALVAFFICRQKASHSRERPSARLS CDIALLPENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGP CDIALLPENRGKNRYNNILPYDASRVKLSNVDDDPCSDYINASYIPGNNFRREYIATQGP 1419 KRYLVSIKVQSAGWISEVVEDSTITWIDRPPPPPPHIRVNEKDVLISKASINFTVNCSWF KRYLVSIKVQSAGMTSEVVEDSTITMIDRPPQPPPHIRVNEKDVLISKSSINFTVNCSWF SNSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKP IRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKEYEELKDVGRNQS Monitoring or modulating Tie-2 tyrosine kinase activity, useful e.g. regulating tumor growth, using vascular-endothelial protein tyrosine phosphatase. ö Length 579; Indels Query Match 28.0%; Score 2937; DB 3; Best Local Similarity 94.3%; Pred. No. 4.3e-198; Matches 546; Conservative 15; Mismatches 18; PLANCK GES FOERDERUNG WISSENSCHAFTEN Disclosure; Page 10-12; 60pp; English 99EP-00108074. WPI; 2000-648932/63 N-PSDB; AAA88865 Sequence 579 AA; 23-APR-1999; (PLAC) MAX 1479 1539 1659 61 121 1599 1719 301 유 à 셤 ò 8 ò g ò ઠે

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                                                                                                                                                                                osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic, gene therapy, diagnostic marker, morbid state, osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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                     541 CVRDVLRAKKLRNEQENPLFPIYENVNPEYHRDAIYSRH 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.7%; Score 1854.5; DB 8 93.0%; Pred. No. 1.4e-121; tive 5; Mismatches 3;
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Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3989; 2449pp; English.
                                                                                       ADQ66828 standard; protein; 609 AA
                                                                                                                                                          Novel human protein sequence #1801
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09-MAY-2003; 2003JP-00131392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
                                                                                                                                    (first entry)
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Isono Y,
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                                                                                                                                                                                                                                                                                                                                               318 DSYNITLSHKGTIKESRVLAPWITETHFKELVPGRLYQVTVSCVSGELSAQKMAVGRTFP 377
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                                                                                                                                                                                                 416 NGSTVPSPVKDIGISTKANSLLISWSHGSGNVERYRLVLMDKGILVHGGVVDKHAISYAF
                                                                                                                                              HGLSPGYLYNLTVMTEAAGLONYRWKLVRTAPMEVSNLKVTNDGSLTSLKVKWQRPPGNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 DKVANLEANNNGRMRSLVVSWSP 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD004582 standard; protein; 336 AA
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                                                                                                                                                                 DRPLSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKEYEELKDVGRNQSCDI
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                    Score 1830; DB 8; I
Pred. No. 2.7e-120;
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17.5%; Scc. 100.0%; Pred. No. ... 0; Mismatches
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identified by this method are useful to treat diseases like diabetic retinopathy, sickle cell anaemia, Paget's disease, mycobacterial infections, systemic lupus erythematosus, myopia, Crohn's disease, psoriasis, rheumatoid arthritis, solid or blood borne tumours and acquired immune deficiency syndrome (AIDS). The invention is useful for the treatment of an angiogenesis mediated disorder or disease. It is also useful in drug design techniques. The present sequence is human HPTPbeta protein catalytic domain.
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Pred. No. 1.7e-110;
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99.4%;
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The invention relates to the three dimensional coordinates of HPTPbeta (also known as HPTP-beta, PTPB, PTPbeta, PTPB or R-PTP-beta) protein. It also relates to a method for the identification of a compound useful for the treatment of an angiogenesis mediated disorder. The compounds identified by this method are useful to treat diseases like diabetic retinopathy, sickle cell anaemia, Paget's disease, mycobacterial infections, systemic lupus erythematosus, myopia, Crohn's disease, psoriasis, rheumatoid arthritis, solid or blood borne tumours and acquired immune deficiency syndrome (AIDS). The invention is useful for the treatment of an angiogenesis mediated disorder or disease. It is also useful in drug design techniques. The present sequence is human HPTPbeta intracellular domain (ICD) truncated protein.
                                                                         Identification of compound useful for treatment of angiogenesis mediated disorder, by using three-dimensional structure of HPTPbeta catalyric domain, and employing structure to design, or select compound that binds HPTPbeta in silico.
                                                                                                                                                                                                            Disclosure; SEQ ID NO 6; 335pp; English.
WPI; 2004-374235/35.
N-PSDB; ADO04583.
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Sequence 312 AA;

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                                                                         1662 DRPLSVHLNLGQKGNRKTSCPIKINQPEGHPMKLQADSNYLLSKEYEELKDVGRNQSCDI 1721
                                                                                                                                                  1722 ALLPENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGPLPG 1781
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16.1%; Score 1690; DB 8; Length 312; 100.0%; Pred. No. 1.9e-110; ive 0; Mismatches 0; Indels (
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Search completed: March 10, 2006, 18:26:36 Job time: 223.124 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new accession number.

If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please members of the public who may encounter UniProt temporary accession numbers.

Ipis bade Blank (nsbio)

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:

March 10, 2006, 18:19:33 ; Search time 285.648 Seconds (without alignments) 4932.432 Million cell updates/sec

US-10-633-742-2 10483 1 MLSHGAGLALWITLSLLQTG......FPIYENVNPEYHRDPVYSRH 1997 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* . Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score		Query Match Length	DB	ΙD	Description
1	10483	100.0	1997	-	PTPRB HUMAN	P23467 homo sapien
7	10226	97.5	1956	~	Q6MZF6 HUMAN	Q6mzf6 homo sapien
m	9124.5	87.0	1998	~	Q8CIW2_MOUSE	mus m
4	6712	64.0	1407	~	Q6ZR19 HUMAN	Q6zr19 homo sapien
S	6103	63.9	1527	~	Q6AWC4 HUMAN	Q6awc4 homo sapien
9	5414	51.6	1102	'n	Q80VN7 MOUSE	Q80vn7 mus musculu
7	3863.5	36.9	1991	~	Q4TC72 TETNG	Q4tc72 tetraodon n
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0	2937	28.0	579	~	Q9JJ07 MOUSE	Q9jj07 mus musculu
10	2772	26.4	771	7	Q86VA4 HUMAN	Q86va4 homo sapien
11	1854.5	17.7	609	7	Q6ZTX7 HUMAN	Q6ztx7 homo sapien
12	1718.5	16.4	723	~	Q9CX77 MOUSE	mius m
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15	1485.5	14.2	1607	~	Q8IRSO DROME	
16	1485.5	14.2	1767	~	Q9W4F5_DROME	
17	1457.5	13.9	1767	~	Q24495_DROME	
18	1379.5	13.2	1406	N	Q9W6V5_CHICK	Q9w6v5 gallus gall
19	1243.5	11.9	1238	-	PTPRJ MOUSE	
20	1243.5	11.9	1238	N	Q541R5 MOUSE	Q541r5 mus musculu
21	1242.5	11.9	1238	N	Q8K3Q2_MOUSE	Q8k3q2 mus musculu
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23	1233.5	11.8	1064	~	Q8SXBZ DROME	_
24	1228.5	11.7	1238	7	Q8CIW9_MOUSE	
25	1221.5	11.7	1216	0	Q62884_RAT	Q62884 rattus norv
26	1204	11.5	1705	~	Q9ERKS MOUSE	Q9erk5 mus musculu
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28	1197	11.4	1711	-	PTPRV RAT	Q64612 rattus norv
29	1103.5	10.5	1188	Ŋ	Q4SDYS_TETNG	
30	1097	10.5	2302	~	O88488_RAT	O88488 rattus norv
31	1003	9.6	442	~	Q4RBH9 TETNG	Q4rbh9 tetraodon n

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ilarity 99.5%; Pred. No. 0;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
4ypochetical protein DKFZp686E13109 (Fragment).
Name=DKFZp686E13109;
Name=DKFZp686E13109;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                      PSPPSLMSFADIANTSLAITWKGPPDWTDYNDFELQWLPRDALTVFNPYNNRKSEGRIVY
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Q6MZF6;
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RY MEDLINE=22220660; PubMed=12234928; DOI=10.1093/emboj/cdf497;

RA WARTINE=22220660; PubMed=12234928; DOI=10.1093/emboj/cdf497;

RA Golding M., Shima D.T., Deutsch U., Vestweber D.;

A Golding M., Shima D.T., Deutsch U., Vestweber D.;

RY TWR-PTP and VB-cadherin ectodomains interact to facilitate regulation of phosphorylation and cell contacts.";

EMBD J. 214885-4895 (2002).

CC EMBL; AY077755; AAL75813.1; -; mRNA.

RSSP; PARGELLUAR LOCATION: Type I membrane protein (By similarity).

RRSI, AY077755; AAL75813.1; -; mRNA.

RRSI, AY077755; AAL75813.1; -; mRNA.

RRSI, AY077755; AAL75813.1; -; mRNA.

RRSI, PARGELLUAR LOCATION: Type I membrane; IEA.

RO; GO:0016781; F:hydrolase activity; IEA.

RO; GO:0016781; F:hydrolase activity; IEA.

RO; GO:0016740; P:protein amino acid dephosphorylation; IEA.

RO; GO:0016470; P:protein amino acid dephosphorylation; IEA.

RITEPTPO; IPR000342; TYR_Phosphatase.

REAM: PF00041; fin3: 16.

RRMRT; SM0019; PTPC; 1.

RRMRT; SM0019; TYR_PHOSPHATASE 1; 1.

RRMRT; SM0019; TYR_PHOSPHATASE 1; 1.

RRMSITE; PS50056; TYR_PHOSPHATASE 2; 1.

RRMSITE; PS50056; TYR_PHOSPHATASE 2; 1.

RRMSITE; PS50056; TYR_PHOSPHATASE 2; 1.

RRMSITE; PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.

RRMSITE; PROSITE; PROGRAMIASE 1; 1.

RRMSITE; PROGRAMIASE 1; 1.
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                                   TKDDFWKMVWEQNVHNI VMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVLPEW
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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larity 85.7%; Pred. No. 0;
Conservative 131; Mismatches 153; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                              Name=Ptprb;
Mus musculus (Mouse)
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	1260 APSPPSIMSFADIANTSLAITWKGPPDWTDYNDFELGWLPRDALTVFNPYNNRKSEGRIV	Oy 1320 YGLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTAIACSWIPPD 1379	Oy 1380 SDFDGYSIECRKMDTQEVEFSRKLEKEKSLLNIMMLVPHKRYLVSIKVQSAGMTSEVVED 1439 [Qy 1440 STITMIDRPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVREADGSD 1499 1441 STITMIDRPPQPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFAVVVREADSMD 1500	OY 1500 ELKPEQOHPLPSYLEYRHASIRVYQTNYFASKCAENPNSNSKSFNIKLGAEMESLGGKR 1559 1501 ELKPEQQHPLPSYLEYRHNASIRVYQTNYFASKCAESPDSSSKSFNIKLGAEMDSLGGKC 1560	Oy 1560 DPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKPLYSDTFFSLPITTESEPLFGA 1619 1561 DPSQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKPLYSDTFFSMPITTESEPLFGV 1620	Oy 1620 IBGVSAGLFLIGMLVAVVALLICRQKVSHGRERPSARLSIRRDRPLSVHLNLGQKGNRKT 1679	Qy 1680 SCPIKINQFEGHFWKLQADSNYLLSKEYEELKDVGRNQSCDIALLFENRGKNRYNNILPY 1739 1681 SCPIKINQFEGHFWKLQADSNYLLSKEYEDLKDVGRSQSCDIALLFENRGKNRYNNILPY 1740	Qy 1740 DATRVKLSNVDDDPCSDXINASYIPCNNFRERYIVTQGPLPGTKDDFWKAVWEQNVHNIV 1799	185	1860 IRHFHYTVWFDHGVPETTQSLIQFVRTYRDYINRSPGAGPTVVHCSAGVGRTGTFIALDR 1	1920 ILQQLDSKDSYDIYGAVHDLR 	OY 1980 IYENVNPEYHRDPYYSRH 1997 	RESULT 4 Q6ZR19 HUMAN D Q6ZR19 HUMAN PRELIMINARY; PRT; 1407 AA.	Post. 2004 (TrEMBLrel. 27, Created) 55-JUL-2004 (TrEMBLrel. 27, Last sequence update) 55-JUL-2004 (TrEMBLrel. 27, Last sequence update) 55-JUL-2004 (TrEMBLrel. 27, Last annotation update)	fragment). Fragment). rrtebrata; Eutel ates; Catarrhin
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61 DTLGAALCPTFRIDNTTYGCNLQDLQAGTIXNFKIISLD-EERTVVLQTDPLPPARFGVS 119	REKTASTTLOVRWIPSSGKVSWYEVOLFDHNNOKLOEVQVQESTTWSQYIFLALITGENSY NIAITAVSGGKRSFSVYINGSTVPSPVKDIGISTKANSLLISWSHGSGNVERYRLALMDK	181 KVAITAVSGEKRSFPVYINGSTVPSFVKDLGISPNPNSLLISWSRGSGNVEQYRLVLMDK 240 240 GILVHGGVVDKHATSYAFHGLSPGYLYNLTVMTEAAGLONYRWKLVRTAPWEVSNLKVTN 299 241 GILVHGGVVDKHATSYAFHKILPGHIVHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	DGSLTSLKVKWQRPGRVDSYNITLSHKGTIKSSRVLAPWITETHFKELVPGRLYQVTVS	CVSGELSAQKWAVGRIFPDKVANLEANNNGRMESLVVSWSPPAGDWEQYRILLEYDSVVL -	LATTVGKEETQYVMDDTGLVPGRQYEVEVIVESGNLKNSERCQGRTVPLAVLQLRVKHAN	BTSLSIMMQTPVAEWEKYIISLADRDLLLIHKSLSKDAKEFTFTDLVPGRKYMATVTSIS	GDLKNSSSVKGRTVPAQYTDLHVANQGMTSSLFTNMTQAQGDVBFYQVLLIHENVVIKNE	SISSETSRYSFHSLKSGSLYSVVVTTVSGGISSRQVVVEGRTVPSSVSGVTVNNSGRNDY	LSVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTITTRSGKY	ENHSFSGERTVEDKVQCVSVSNSARSDYLKVSWVHATGEFDHYEVTIKNKNNFIQTKSIP	KSENECVPVQLVPGRLYSVTVTTKSGQYEANEQCNGRT1PEPVXDLTLRNRSTEDLHVTW	840 SGANGDVDQYELQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSA 899	900 FIEGFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVF 959 	960 EHTFHRLEAGEQYQIMIASVSGSLKNQINVVGRTVPASVQGVIADMAYSSYSLIVSWQKA 1019 	1020 AGVAERYDILLITENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQT 1079 	1080 BGRTVPAAVTDLRITENSTRHLSFRWTASEGELSWYNIFLYNPDGNLOERAQVDELVQSF.1139

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955 MKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEGFTVPSAVKNIHISP 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQTEGRTVPAAVTDLRITENS 1097
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                                                               SVSNSARSDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIPKSENECVFVQLVPGRLYS
                                                                                                                                                                                                                                            858 MKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEGFTVPSAVKNIHISP
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                 SVSNSARSDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIPKSENECVFVQLVPGRLYS
                                                                                                                                    VTVTTKSGQYEANEQGNGRTIPEPVKDLTLRNRSTEDLHVTWSGANGDVDQYEIQLLFND
                                                                                                                                                                  VIVITKSGQYEANEQGNGRIIPEPVKDLILRNRSIEDLHVIWSGANGDVDQYEIQLLFND
                                                                                                                                                                                                                                                                                                                                                  918 NGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVFEHTFHRLEAGEQYQIMIA
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TISSUE=Endometrium;
The German cDNA Consortium;
The German cDNA Consortium;
The German cDNA Consortium;
A Fobo G., Han M., Wiemann S.,
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BK647238; CAHIO1386.11; -; mRNA.
InterPro; IPR003961; FN III.
R InterPro; IPR000772; Ricin_B lectin.
R Pfam; PF00061; fn3; 15.
R Pfam; PF00061; fn3; 14.
R PROSITE; PS50831; RN3; 14.
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Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence upd
25-OCT-2004 (TrEMBLrel. 28, Last annotation u
pothetical protein DKFZp686E2262 (Fragment)
Name-DKFZp686E2262;
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QGAWC4;
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                                                                                                Kanchori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanai H., Watanabe S., Ishidas S., Ono Y., Hotuta T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
Ishil S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshina A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

R. MAL28562; BAC87502.1;
R. MEND. PRO03651; F. MENA.
GO: GO:0005529; F:sugar binding; IEA.
R. InterPro; IPR00361; F. III.
R. FFRON, PRO0361; F. III.
R. SMART; SM00060; FN3; 14.
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NON_TER 1407 1407
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Matches 1288; Conservative
NCBI_TaxID=9606;
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SFRWTASEGELSWYNIFLYNDDGNLQERAQVDPLVQSFSFQNLLQGRWYKMVIVTH 1157
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ENT. TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
ENT. TISSUES BARNERS BARNE
SEPATTKOHKFEDLTPGKKYKIQILTVSGGLFSKEAQTEGRTVPAAVTDLRITENS 1097
                                                                                                                                                                                                                                                                                                                                                                        SNESFIFGRTVPASVSHLRGSNRNTTDSLWFNWSPASGDFDFYELILYNPNGTKKE 1217
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heria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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87; F:hydrolase activity; IEA.
25; F:protein tyrosine phosphatase activity; IEA.
770; P:protein amino acid dephosphorylation; IEA.
R003961; FN III.
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TrEMBLrel. 24, Last sequence update)
TrEMBLrel. 26, Last annotation update)
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1856 AHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFI 1915
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Mauceli B., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Kellis M., Volff JN., Guigo R., Zody M.C., MeBwan P., Bosak S.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lander V., Schachter V., Quetier P., Saurin W., Scarpelli C.,
Wincker P., Lander B.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                 1736 ILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGPLPGTKDDFWKMVWEQNV
                                     841 ILPYDASRVKLCNVDDDPCSDYINASYIPGNNFRREYIATQGPLPGTKDDFWKMAWEQNV
                                                                             HNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVLPEWTIREFKICGEEQLD
                                                                                              HNIVMVIQCVEKGRVKCDHYWPADQDPLYYGDLILQMVSESVLPEWIIREFKICSEEQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Čraniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF7048, whole genome shotgun sequence.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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EMBL, CAAE01007048; CAF69510.1; -; Genomic_DNA.
InterPro; IPR003961; FN III.
InterPro; IPR003595; PTPC morif.
InterPro; IPR000387; TYR_Dhosphatase.
InterPro; IPR000242; TYR_PP.
Pfam; PF000041; fn3; 14.
Pfam; PF00102; Y phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
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ORFNames=GSTENG0003440001;
Tetraodon nigroviridis (Green puffer).
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SMART; SM0194; PTPc; 1.
SMART; SM00404; PTPc_motif; 1.
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Q4TC72;
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NUCLEOTIDE SEQUENCE.
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Pfam; PF0102; Y_phosphatase; 1.
PRINTS; PR00100; PRYPHPHTASE.
SMART; SM00060; FN3; 6.
SMART; SM00194; PTPc; 1.
PROSITE; PS50853; FN3; 6.
PROSITE; PS50056; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
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                                                                     Length 1991;
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36.9%; Score 3863.5; DB 2; Length
Best Local Similarity 41.1%; Pred. No. 7.5e-216;
Matches 831; Conservative 314; Mismatches 611; Indels
                                                     1991 AA; 214280 MW; AE8CE4629DD27A78 CRC64;
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PROSITE; PS50853; FN3; 14.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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1451 1391 1511 1707 1717 1767 1777 1827 1887 1128 WVRLSSSS----SSVPSAVSSLEAESSGQTDGLVVSWRHGDGSWSGYQVLLCDASGATVA 895 AVSGRTAPARVTALQADNQHTAHSLTVSWERPAGLHDAYRLQLLDRGGAVLAQRTLPADS KOHKFEDLIPGKKYKIQILIVSGGLFSKEAQTEGRIVPAAVTDLRITENSTRHLSFRWTA |:| : |:: ||: SDGHVDVYHVSLYSVPEPAADGRQVGSSFRRPSGEPCGGLTEGRGGGGRLRVRRPAGGKP -- ELSNESFIFGRTVPASVSHLRGSNRNTTDSLWFNWSPASGDFDFYELILYNPNG-TKK SGDSWK----TYSKPIFGSVRTKPDKIQNLHCRPQNSTAIACSWIPPDSDFDGYSIECRK PPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVREADGSDELKPEQOHPLPS YLEYRHNASIRVYQTNYFASKCAENPNSNSKSFNI------KUGAEMESLGGKRD TE----SEPLFGAIEGVSAGLFLIGMLVAVVALLICROKVSH-FRREYIVT GGPLPGTKDDFWKMWWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGD NVVGRTVPASVQGVIADNAYSSYSLIVSWQKAAGVAERYDILLLTENGILLRNTSEPATT APPAGGELEPGHE----ORLLHARONRSV---HTGGNALAPPPPLVAGGHMTPGVSHAFT SLAITWKGPPDWTDYNDFELOWLPRDALTVFNPYNNRKSEGRIVYGLRPGRSYOFNVKTV MDTQEVEPSRKLEKEKSLLNIMMLVPHKRYLVSIKVQSAGMTSEVVEDSTITMIDRPPPP -GRERPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKEY LILOMLSESVLPEWTIREFKICGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTV RDYINRSPGAGPTVVHCSAGVGRTGTF1ALDR1LQQLDSKDSVD1YGAVHDLRLHRVHMV ----RAQVDPLVQSFSFQNLLQGRMYKMVIVTHSG-----SEGELSWYNI FLYN----------PDGNLQE-----

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1479 SDTNGAVKYFTVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQTNYFASKCAENPN 1538
                                   775
                                                                   617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDINGAVGYFAVVVREADSMDELKPEQQHPLPSYLEYRHNASIRVYQTNYFASKCAESPD 120
                                                                                                                                LYSVVVTTVSGGISSRQVVVEGRTVPSSVSGVTVNNSGRNDYLSVSWLVAPGDVDNYEVT 677
                                                                                                                                                                                                737
     IISLADRDLLLIHKSLSKDAKEFTFTDLVPGRKYMATVTSISGDLKNSSSVKGRTVPAQV 557
                                                                                                                                                                                                                                -----RIVPDKVQGV 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                     TDLHVANQGMTSSLFTNWTQAQGDVEFYQVLLIHENVVIKNESISSETSRYSFHSLKSGS
                                                                   TDLHVANQGMTSSLFTNWTQAQGDVEFYQVLLIHENVVIKNESISSETSRYSFHSLKSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1419 KRYLVSIKVQSAGMISEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KRYLVSIKVQSAGMTSEVVEDSTITMIDRPPQPPPHIRVNEKDVLISKSSINFTVNCSWF
                                                                                                                                                                                                LSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTITTRSGKYENHSFSQERTVPDKVQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Vascular endothelium;
Fachinger G., Detusch U., Risau W.;
Functional interaction of vascular endothelial protein tyrosine
phosphatase with the angiopoletin receptor Tie-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ensembl, ENSMUSCO000020154; Mus musculus.
MGI; MGI:97809; Ptprb.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 579;
                                                                                                                                                                                                                                                              SVSNSARSDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIPKSE 782
                                                                                                                                                                                                                                                                                  SVSNSARSDYLRVSWVHATGDPDHYEVTIKNKONFIQTKAFPSQK 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Receptor-type protein tyrosine phosphatase (Fragment).
                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
28.0%; Score 2937; DB 2;
Best Local Similarity 94.3%; Pred. No. 1.2e-162;
Matches 546; Conservative 15; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                               579 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00194; PTPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                     InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000225; Tyr_PP.
Pfam; PF00102; Y phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                          01-00T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 0:0-0(1999).
EMBL; AF157628; AAF80346.1; -; mRNA.
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                           Q9JJ07 MOUSE PRELIMINARY;
Q9JJ07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muridae: Murinae: Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Ptprb;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 YGCNLQDLQAGTIYNFKIISLDEERTVVLQTDPLPPARFGVSKEKTTSTSLHVWWTPSSG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVPGRQYEVEVIVESGNLKANSERCQGRTVPLAVLQLRVKHANETSLSIMMQTPVAEWEKY 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVTSYEVQLFDENNQKIQGVQIQESTSWNEYTFFNLTAGSKYNIAITAVSGGKRSFSVYT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGSTVPSPVKDIGISTKANSLLISWSHGSGNVERYRLMLMDKGILVHGGVVDKHATSYAF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGLSPGYLYNLTVWTEAAGLQNYRWKLVRTAPMEVSNLKVTNDGSLTSLKVKWQRPPGNV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSYNITLSHKGTIKESRVLAPWITETHFKELVPGRLYQVTVSCVSGELSAQKMAVGRTFP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKVANLEANNNGRMRSLVVSWSPPAGDWEQYRILLFNDSVVLLNITVGKEETQYVMDDTG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVPGRQYEVEVIVESGNLKNSERCQGRTVPLAVLQLRVKHANETSLSIMWQTPVAEWEKY 497
                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSYNITISHKGTIKESRVLAPMITETHFKELVPCRLYQVTVSCVSGELSAQKAVGRTFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGCNLODLOAGTIYNFKIISLDEERTVVLQTDPLPPARFGVSKEKTTSTGLHVWWTPSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTGLAEPERCNFTLAESKASSHSVSIQWRILGSPCNFSLIYSSDTLGAALCPTFRIDNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                       Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR74954-6, CAH18347-1; -; mRNA.
GO, GO:0005529; F:sugar binding; IEA.
InterPro; IPR003961; FN III.
Pfam; PF00041; fn3; 8.
Fam; PF00041; fn3; 8.
Fam; PF00061; FN3; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 919;
4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. TseQUENCE 919 AA; 102458 MW; 7723EFDBC03CEED0 CRC64;
                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686H15164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.6%; Score 3413; DB 2;
llarity 87.5%; Pred. No. 4.2e-190;
Conservative 4; Mismatches 4;
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                                                                                                 PRT;
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PROSITE, PS50231; RICIN B LECTIN; 1.
                                                                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE.
TISSUE=Uterus endothel;
The German cDNA Consortium;
                                                                                            Q68D73 HUMAN PRELIMINARY;
Q68D73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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Matches
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Homo sapiens (Human)
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE
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                        IISSUE=Spleen;
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Q6ZTX7_HUN
SORREDDREERS
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WEDLINE-22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.F. Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K.F. Farmer A.A., Rubin G.M., Hong L.,

B Arablecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahe, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Schnertfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.B.,

B Schnercth A., Schein J.E., Jones S.J.M., Marra M.A.,

B A Maria M.A., Schein J.E., Jones S.J.M., Marra M.A.,

B A Maria M.A., Robert M. M. A., Marra M.A.,

R Roderstine M. A., Schein J.E., Jones S.J.M., Marra M.A.,

B A Maria M.A., Schein J.E., Jones S.J.M., Marra M.A.,

R Roderstine M. M. A., Marra M.A.,

R Roderstine M. M. Marra M.A.,

R Roderstine M
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                        SNSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKP 1598
                                                                                                                             LYSDTFFSLPITTESEPLFGAIEGVSAGLFLIGMLVAVVALLICRQKVSHGRERPSARLS 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                             LPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVL 1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEWTIREFKICGBEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAG 1898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVYLHQ 1958
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                             241 IRRDRPLSVHLNIGQKGNRKTSCPIKINQPEGHFMKLQADSNYLLSKBYEDLKDVGRSQS
                                                   I RRDR PLSVHLNLGQKGNRKTSCPI KI NQPEGHFMKLQADSNYLLSKEYEELKDVGRNQS
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
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Q86VA4;
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NCBI_TaxID=9606;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                           Length 771;
Director MGC Project;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051329; AAH51329.1; mRNA.
REnsembl; ENSG00001027329; Homo sapiens.
R CO; GO:0005529; F:sugar binding; IEA.
R InterPro; IPR000772; RiGin_Blectin.
R Pfam; PF00041; Fin3; 6.
R Pfam; PF000641; Fin3; 6.
R Pfam; PF000652; Ricin_Blectin; 1.
R Pfam; PF000651; Ricin_Blectin; 1.
R Pfam; PF000551; Ricin_Blectin; 1.
R PROSITE; PS50853; FN3; 6.
R PROSITE; PS50853; RN3; 6.
R PROSITE; PS50851; RICIN B LECTIN; 1.
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last senotation update)
CDNA FLJ4133 fis, clone THYMU2008725, highly similar irrosine PHOSPHATASE BETA (EC 3.1.3.48).
                                                                                                                                                                                                                                                                                                                      Query Match 26.4%; Score 2772; DB 2; Best Local Similarity 99.4%; Pred. No. 8.1e-153; Matches 533; Conservative 2; Mismatches 1;
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QEZTX7;
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NUCLECATION SEQUENCE.

X MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

X MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

X Awai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Pukunishi Y., Komon H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

X Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Achimal D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X Khehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

X Sakai K., Okido T., Puruno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Browstein M.J., Bult C., Pletcher C., Fullita M., Mazarelli J., Mombaerts P.,

A Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

R Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nayashi, Jaki Y.,

Nayashi, Jaki 
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                           MEDLINE-99279253; PubMed-10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hayashizaki Y.; Hispahizaki Y.; Hispahicaki Y.; Hispahicaki Y.; Hispahicaki Y.; Hispahicaki Y.; Hispahicaki Y.)
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Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatusu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kogas S., Kurihara C.,
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Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
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Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
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"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
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The FANTOM Consortium,
STRAIN=C57BL/6J; TISSUE=Head;
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295
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               A Arite M., Musashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arite M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamateu A., Ishii S., Yamamoto J., A Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Amashita H., Matsuo K., Naganera Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; NEDO human CDNA sequenching project."; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

I. Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

R. MILETPED, ISPRO03961; FN III.

R. InterPro; IPR003961; FN III.

R. Pfam. PROMO41. fn3. 4
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2014 (TrEMBLrel. 26, Last annotation update)
Mus musculus 14, 12 days embryo head CDNA, RIKEN full-length enriched
library, clone:3230402H02 product:hypothetical Fibronectin type III
domain/Ricin B lectin domain containing protein, full insert
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Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.7%; Score 1854.5; DB 2; Length 609; 93.0%; Pred No. 1.9e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1854.5,
Pred. No. 1.9e-99;
Pred. No. 1.9e-99;
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Pfam; PF00052; Ricin Blectin; 1.
SMART, SM00060; Fn3; 4.
PROSITE; PS50231; RICIN BLECTIN; 1.
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NCBI_TaxID=10090;
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NUCLEOTIDE SEQUENCE.
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PKSENECVFV--QLVPGRLYSVTVTTKSGQYEANE-----QGNGRTIPEPVKDLTLRNR 830
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                                                                                                                                                                                                                                                                                                                                                                                 446 INGSTVPSPVKDLGISPNPNSLLISWSRGSGNVEQYRLVLAMDKGAIVQDTNVDRRDISYA 505
                                                                                                                                                                                                                                                                                                                                                                                                                            266 ETGVAEQVKCNFTLLESRVSSLSASIQWRTPASPCNFSLIYSSDTSGPMWCHPIRIDNFT 325
                                                                                                                                                                                                                                                                                                                        GKVTSYEVQLFDENNQKIQGVQIQESTSWNEYTFFNLTAGSKYNIAITAVSGGKRSFSVY 196
                                                                                                                                                                                                                                                                                                                                                                     TNGSTVPSPVKDIGISTKANSLLISWSHGSGNVERYRLMLMDKGILVHGGVVDKHATSYA 256
                                                                                                                                                                                                                                                                                                                                                                                                                FHGLSPGYLYNLTVMTEAAGLQNYRWKLVRTAPMEVSNLKVTNDGSLTSLKVKWQRPPGN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDSYNITLSHKGTIKESRVLAPWITETHFKELVPGRLYQVTVSCVSGELSAQKMAVGRTF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDKVANLEANNNGRMRSLVVSWSPPAGDWEQYRILLFNDSVVLLNITVGKEFTQYVMDDT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGCNLQDLQAGTIYNFKIISLD-EERTVVLQTDPLPPARFGVSKEKTTSTGLHVWWTPSS
                                                                                                                                                                                                                            QTGLAEPERCNFTLAESKASSHSVSIQWRILGSPCNFSLIYSSDTLGAALCPTFRIDNTT
                                                                                                                                                                                                       Gaps
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Bukaryota; Metazoa; Atthopoda; Hexapoda; Insecta; Pterygota;
Neoptera; Budopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                      1;
                                                                                                                                                                                Length 723;
                                                                                                                                                                              / Match 16.4%; Score 1718.5; DB 2; Length Local Similarity 72.6%; Pred. No. 2.2e-91; les 326; Conservative 50; Mismatches 72; Indels
        Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, AK019450; BAB31726.1; -; mRNA.
BRRBL, AK019450; BAB31726.1; -; mRNA.
BRISHDL); RNSWUGGO000020154; Mus musculus.
MGI; MGI:97809; Ptprb.
GO; GO:005529; F:Sugar binding; IRA.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
Pfam; PF00062; Ricin B lectin.
SMART; SM00060; FN3; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                      PROSITE; PS50853; FN3; 5.
PROSITE; PS5021; R.CIN B.LECTIN; 1.
Hypotherical protein: Lectin.
SEQUENCE 723 AA; 79341 MW; 184FF7E96B32EESF CRC64;
                                                                                                                                                                          DB 2;
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Q7PQLO;
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
BNSANGPO0000013354 (Fragment).
ORFNames=ENSANGG0000010865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLVPGRQYEVEVIVESGNLKNSERCQGRT
Hayashizaki Y.;
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ETHPKELVPGRLYQV------TVSCVSGELSAQKMAVGRTFPDKVANLEA- 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443 QYEVE------VIVESGNLKNSERCQGRTVPLAVLQLRVKHANETSLSIMWQT--P 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSVKGRTVPAQVTDLHVANQGMTSSLF-TNWTQAQGDVEF--YQVLLI---HENVVIKN 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SW-PASGD-----VTL------KPLPVKQLQSYTDSKTGVITISWK--- 384
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                                                                                                                                                                                                                                .; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                659 YLSVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTITTRSGK
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                                                                                          EMBL/GERNAINK/DUBU WIDLE GENOUNE BLOUGHLING, CLEAR EMBL/ARABO1008800, EAA08669.3; -; Genomic_DNA.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0016780; F:hematopoietin/interferon-class (D200-domain. ..;

R GO; GO:0016780; F:homatopoietin/interferon-class (D200-domain. ..;

R GO; GO:0016780; F:protein tyrosine phosphatase activity; IEA.

R InterPro; IPR0003962; FNIII_subd.

R Fam; PF000104; FNIYPEIII

R RRINTS; RR000104; FNIYPEIII

R RART; SM00104; FNIYPEIII

R SMART; SM00104; FNIYPEIII

R SMART; SM00104; FNIYPEIII

R RROSITE; FS50833; FNI II.

R RROSITE; PS50056; TYR_PHOSPHATASE_2; I.

R RROSITE; PS50056; TYR_PHOSPHATASE_PTP; I.
Submitted (APR 2004) to the EMBL/GenBank/DDBJ databases.
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1506;
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14.9%; Score 1566; DB 2;
Best Local Similarity 29.5%; Pred. No. 6e-82;
Matches 512; Conservative 263; Mismatches 583;
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Cell 67:661-673(1991).
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                                                                                                                                 1008 SSYSLIVSWQKAAGVAERYDILLLTENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILT 1067
                                                                                                                                                                   1068 VSGGLFSKEAQTEGRTV-PAAVTDLRITENSTRHLSFRWTASEGELSWYNIFLY---NPD 1123
                                                                                                                                                                                                                                                                                                                                                                                   TQEVEFSRKLEKEKSLLNIMMLVPHKRYLVSIKVQSA-GMTSEVVEDSTITMIDRPPPPP 1452
                                                                                                                                                                                                                                                                                                                                                                                                                     1453 PHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVREADGSDELKPEQQHPLPSY 1512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKPHTAYRISIRAFTQLFDEDLKEFTKPLYSDTFFSLPITTESEPLFGAIEGVSAGLFLI 1630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMLVAVVALLICRQKVSHGRERPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEG 1690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFMKLQADSNYLLSKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPYDATRVKLSNVD 1750
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                                                                                                                                                                                                                                         -LRGSNRNTTDSLWFNWSPA---SGDFDFYELILYNPNGTKKE---NWKDKDLTEWRFQG 1231
                                                                                                                                                                                                                                                                                                                                                1348 FGSVRTKP-----DKIQNLHCRPQNSTAIACSWIPPDSDFDG------YSIECRKMD 1393
           464
                                                            TISGDVQQS--AFIEGFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQ 947
                                                                              522 AVSHGLRSEPHSYFQA-VYPNPPRNMTIE-KVTSNSVLVHWKP--PERSEFTEYSIRYRT 577
                                                                                                                 330 VVIVNNMHTRDMVTLSYTPTPQQSSKFDLYRFSLGDPSIPDKEKLANDTDRKVT---FTG 786
                                                                                                                                                                                                                                                                                                                                900
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                                    STEDLHVTW-SGANGDVDQYEIQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVL
                                                                                                                                                   ------VTDMTPGEKYTIQVNT
                                                                                                                                                                                                                 LVPGRKYVLWVVTHSGDLSNK-VTAESRTAPSPPSLMSFADIANTSLAITWKGPPDWTDY
                                                                                                                                                                                                                                                                                      RDVQSYSVWPPYQVIEPYYPFK----NSSVEDFTI--GTE-----NCDAKKTGYCNGP
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Amanatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Holf R.A., Forans C.A., Galle R.F.,
A Adams M.D., Celniker S.E., Holf R.A., Forans C.A., Galle R.F.,
A decorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A brandon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Pfeiffer B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Bullke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Burtis K.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Bobler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harrey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kanison J.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kanison J.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kanison D.,
Lei Y., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B.L., McIntosh T.C., McLeod M.P., McPherson D.,
Murklow G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Murxy D.M., Nelson D.E.,
Nelson D.R., Nelson D.R., Nixon K., Nusskern D.R., Pacieled J.M.,
1331 KCDHYWPHDTVPVYYGDIKVTLLNDSHYPDWVITEFMMTRGEQQ----RIIRHFHFTTWP 1386
                                                                                                                                                  DHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRILQQLDSKDS 1929
                                                                                                                                                                                                                                                                                                           1444
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                                                                                                                                                                                                                                      Tian S.-S., Tsoulfas P., Zinn K.; "Three receptor-linked protein-tyrosine phosphatases are selectively expressed on central nervous system axons in the Drosophila embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1930 VDIYGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLRARKLRSEQENPLFPIYEN 1983
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MEDLINE=92034988; PubMed=1657401; DOI=10.1016/0092-8674(91)90062-4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTP10_DROME STANDARD; PRT; 1631 AA.
P35992; Q86NN9; Q81R87; Q9VYW1;
01-JUN-1994 (Rel. 29, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang X., Seow K.T., Bahri S.M., Oon S.H., Chia W., "Two Drosophila receptor-like tyrosine phosphatase genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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acid dephosphorylation; IDA

protein amino

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED unstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shenert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiames I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodgeg T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodgeg T., Worley K.C., Wu D., Yang G., Zhong I., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zho X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Encosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Berkeley; TISSUB-Embryo; Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G. Miranda A., Mungall C.J., Nunco J., Pacleb J.M., Paragas V., Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENOME REANNOTATION, AND ALTERNATIVE SPLICING.
MEDLINE=22426069; PubMed=1253752;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Haradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.,

    -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein

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TISSUE SPECIFICITY: Selectively expressed in anterior commissum
and its junctions with the longitudinal tracts.
SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
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SIMILARITY: Contains 12 fibronectin type-III domains.
SIMILARITY: Contains 1 tyrosine-protein phosphatase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bold=P35992-4; Sequence=VSP_015264, VSP_015265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P35992-2; Sequence=VSP_005143, VSP_005144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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IsoId=P35992-3; Sequence=VSP_015266;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P35992-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           systematic review.";
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Query Match 14.9%; Score 1561.5; DB 1; Length 1631; Best Local Similarity 27.9%; Pred. No. 1.3e-81; Matches 514; Conservative 271; Mismatches 633; Indels 421; Gaps
                                                                                                                PROSITE; PS50853; FN3; 11.
PROSITE; PS00333; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.
Alternative splicing; Glycoprotein; Hydrolase; Protein phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                   Potential
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Extracellular (Potential).
Potential.
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Phosphocysteine intermediate
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Fibronectin type-III 1.
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Fibronectin type-III
Fibronectin type-III
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GQQVQLDENG ->
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N-linked
       InterPro; IPR000282; Cytok receptor_2.
InterPro; IPR003961; FN III.
InterPro; IPR003962; FNIII_subd.
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                        InterPro; IPR003962; FnIII subd.
InterPro; IPR00387; TYR phosphatase.
InterPro; IPR000387; TYR PP.
Pfam; PF001041; Fn3; 10.
Pfam; PF00102; Y phosphatase; 1.
                                                                           PRINTS; PROOD14; FNTYPEIII.
PRINTS; PROOTOO; PRTYPHPHTASE.
SMART; SMOOD60; FN3; 11.
SMART; SMOO194; PTPC; 1.
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SIGNAL 1 42
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74;

---KLVRTAPMEVS--NLKVTNDGSLT 304

265 LYNLTVMTEAAGLQ-----NYRW--

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Base; FBgn0004370; Ptp10D. GO:0004725; F:protein tyrosine phosphatase activity; IDA.

FlyBase; GO; GO:00 Ensembl;

CG1817; Drosophila melanogaster

PIR, D41214; D41214. HSSP; P10586; 1LAR.

EMBL; AE003486; AAF48072.2; -; Genomic_DNA. EMBL; AE003486; AAN09638.1; -; Genomic_DNA. EMBL; BT004474; AAO42638.1; -; mRNA.

EMBL; M80465; AAA28484.1; -; mRNA. EMBL; M80538; AAA28952.1; -; mRNA. EMBL; AE003486; AAF48072.2; -; Genc

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MEDLINE=22426070; PubMed=12537573;
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                                                                                                                 - SUBCELLULAR LOCATION: Type I membrane protein (By similarity). BL; AE003432; AAN09133.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.2%; Score 1485.5; DB 2; Length 1607;
larity 29.2%; Pred. No. 3.3e-77;
Conservative 269; Mismatches 687; Indels 197;
                                                                                                                                                                                                                                     R GO; GO:0016021; C:1016gral to membrane; IEA.

R GO; GO:0016021; C:1016gral to membrane; IEA.

R GO; GO:0016021; C:1016gral to membrane; IEA.

R GO; GO:0006470; F:1020cein tyrosine phosphatase activity; IEA.

R GO; GO:0006470; F:1020cein amino acid dephosphorylation; IEA.

R InterPro; IPR003961; FNIII subd.

R InterPro; IPR003961; FNIII subd.

R InterPro; IPR003961; FNIII subd.

R InterPro; IPR003961; TYP_PP.

R Pfam; PF00011; fn3; 10.

R Pfam; PF000102; Y phosphatase; 1.

R PRINTS; PR00104; FNTYPRIII.

R PRINTS; PR00106; FNIYPRHHTASE.

R SMART; SM00194; FTPC; 1.
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SEQUENCE 1607 AA; 182285 MW; 6CAF554E61A27F45 CRC64;
"Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE PTP; 1.
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FlyBase; FBgn0004368; Ptp4E.
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Matches 475;
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999	OGVIADNAYSSYSLIVSWQKAAGVAERYDILLIFENGILLRNTSEPATTKQHKF 1052 :	
1053	EDLIPGKKYKIQILTVSGGLFSKEAQTEGRTVPAAVTDLRITENSTRHLSFRWTASEGEL 1112 	
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1163 794	NESFIFGRIVPASVSHLRGSNRNTIDSLMFNWSPASGDFDFYELILYNP 1211 : : : :	
1212	NGTKKENWKDKDLTEWRFQGLVPGRKYVLWVVTHSGDLSN-KVTAESRTAPSPPSLMSFA 1270 TIKDKEKLANDTERKLSFSGLTPGKLYNVTVWTVSGGVASLPVQRLYRLHPLPISDLKAI 909	
1271	DIANTSLAITWKGPPDWTDYNDFELQWLPRDALTVFNPYNNRKSEGRIVYGLRPGRSYQF 1330 :	
1331	NVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTAIACSW 1375	
1376	-IPPDSDFDGYSIECRKMDTQEVEFSRKLEKEKSLLNINMLVPHRRYLVSIKVQSA- 1430 	
1431	GMTSEVVEDSTIIMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTV 1490	
1491		
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1844	REFKICGEEQLDAHRLIRHFHYTWPDHGVPETTOSLIOFVRTVRDYINRSPGAGFT 1900	
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US-10-633-742-2 10483 1 MLSHGAGLALMITLSLLQTG......PPIYENVNPEYHRDPVYSRH 1997 Title: Perfect score:

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 572060 segs, 82675679 residues Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued Patents AA:*

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2. /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 8833, Ap Sequence 8834, Ap Sequence 8835, Ap	883 883 883	Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli	Sequence 15, Appl Sequence 15, Appl Sequence 4, Appli	Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli
US-09-949-016-8833 US-09-949-016-8834 US-09-949-016-8835	US-09-949-016-8836 US-09-949-016-8837 US-09-949-016-8838	US-08-348-006B-5 US-08-800-825A-5 US-09-158-657-5	PCT-US94-10166-5 US-08-447-464-3 US-08-716-679-3	US-08-685-992-15 US-09-144-925-15 US-08-652-971-4	US-08-991-258A-4 US-08-769-399-4 US-08-991-953A-4
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796	796	761.5 761.5 761.5	761.5 748.5 748.5	744.5 744.5 719.5	719.5 719.5 719.5
3 5 8 3 6 8	33 33 33 33 33	3.3.4 3.5.4	7 8 6 5 7 8 6 5	4 4 4 0 1 2	4 4 4 6 4 6

ALIGNMENTS

RESULT 1

1016-6 10
Sequence 6275, Application US/09949016

1381 DFDCYSIECRKMOTOEVEESRILAINAGUVPHKRYLVSIKVQSAGATGEVVDBD 1441 TITMIDRPPPPPHIRVNEKOYLISKSSINFTWCSAFFSDTWGAYKTTVVVRBAGSSDE 1500 1441 TITMIDRPPPPPHIRVNEKOYLISKSSINFTWCSAFFSDTWGAYKTTVVVRBAGSSDE 1500 1441 TITMIDRPPPPPHIRVNEKOYLISKSSINFTWSCSAFFSDTWGAYKTTVVVRBAGSSDE 1500 1441 TITMIDRPPPPPHIRVNEKOYLISKSSINFTWSCSAFFSTRIKLGABMESIGGKRD 1560 1561 PTOQUECCOPLESTLEYRINASIRVYQTVYPASKCAENPNSNSKSFNIKLGABMESIGGKRD 1560 1561 PTOQUECCOPLKPHTAYRISIRAPTOLEDELKEFTKPLYSDTPFSLFITESSPLEGAI 1620 1561 PTOQUECCOPLKPHTAYRISIRAPTOLEDELKEFTKPLYSDTPFSLFITESSPLEGAI 1620 1661 PTOQUECCOPLKPHTAYRISIRAPTOLEDELKEFTKPLYSDTPFSLFITESSPLEGAI 1620 1661 PTOQUECCOPLKPHTAYRISIRAPTOLEDELKEFTKPLYSDTPFSLFITESSPLEGAI 1620 1661 PTOQUECCOPLKPHTAYRISIRAPTOLESTERREPARANSTYS 1660 1661 1670 167	RESULT 2 US-09-949-016-8049 is Sequence 8049, Application US/09949016 is Patent No. 681239 is General No. 681239 is General INFORMATION: is APPLICATION VENTEN, J. Craig et al. it TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF it TILE REPRENCE: LOOG-10-10-10-10-10-10-10-10-10-10-10-10-10-
	HTFHRLEAGEOYQIMLASVSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA HTFHRLEAGEOYQIMLASVSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA HTFHRLEAGEOYQIMLASVSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA HTFHRLEAGEOYQIMLASVSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA GVAERYDILLITENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQTE GRTVPAAVTDLRITENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQTE GRTVPAAVTDLRITENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQTE GRTVPAAVTDLRITENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQTE GRTVPAAVTDLRITENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQTE GRTVPAAVTDLRITENGILLRNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAQTE GRTVPAAVTDLRITENGTRHLSFRWTASEGELSWYNIFLYNPDGNLQBRAQVDPLVQSFS FQNLLQGRWYKWVIVTHSGELSNESFIFGRITVPASVSHLRGSNRNTTDSLWFNWSPASGD FPFYELILYNPNGTKKENWKDKOLTEWRFQGLVPGRKYYLWWVTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFQGLVPGRKYYLWWVTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFQGLVPGRKYYLWWVTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFQGLVPGRKYYLWWVTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFQGLVPGRKYYLWWVTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFQGLVPGRKYYLWWYTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFQGLVPGRKYYLWWYTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFQGLVPGRKYYLWWYTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFPQGLVPGRKYYLWWYTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFPQGLVPGRKYYLWWYTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFPQGLVPGRKYYLWWYTHSGDLSNKYTAESRTA FDFYELILYNPNGTKKENWKDKOLTEWRFPQHLPRODALTVFRPYNNRKSEGRITY FDFYELILYNPNGTKKENWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTALACSWIPPDS GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTALACSWIPPDS GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTALACSWIPPDS GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTALACSWIPPDS GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTALACSWIPPDS GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTALACSWIPPDS GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTALACSWIPPDS GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTALACSWIPPDS GLRPGRSYQFNVKTVSGSSKTTRPDFILLITHINGNTHANTARTALNTHRFILLITHINGNTHANTARTALNTHANTARTALNTH

6 B 6 B 6 B 6 B 6 B

933 GRITORANTENSTRIASTRIASPECRISWINIPLINIPUM	RESULT 3 US-08-201-697-16 Sequence 16, Application US/08201697 Sequence 16, Application US/08201697 Patent No. 5705623 GENERAL INFORMATION: APPLICANT: Thomas, Roger C. APPLICANT: Thomas, Peedikayil E. TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein TITLE OF INVENTION: NUMBER OF SEQUENCES: 17
	961 HTFHRLEAGEOYOLMIASVSGSLKNOINVVGRTVPASVQCVIADNAVSSYSLIVSWQKAA 1020

8 4 8 6 8 6 8 6 8

6 8 6 8 6 8 6 8 6 8 6 8 6

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COUNTRY: USA
ZIP: 02421-4799
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.19
Best Local Similarity 99.2°
Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino ac
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1742 TRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGPLPGTKDDFWKWVWEQNVHNIVMV 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1802 TQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVLPEWTIREFKICGEEQLDAHRLIR 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1862 HFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRIL 1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGPLPGTKDDFWKAYWEQNVHNIVMV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 HFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRIL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PIKINQFEGHFMKLQADSNYLLSKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPYDA 60
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US-08-992-14

Sequence 14, Application US/08685992

Patent No. 5912138

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA
                                                                                                                                           COMPUTER PALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,697
FILING DATE: 25-FEB-1994
CLASSIFICATION: SAND
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryb A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-UM 9783
TELECOMMUNICATION INFORMATION:
TELEFRAX: (619) 535-8049
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                    E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
                                                            CITY: San Diego
STATE: California
COUNTRY: USA
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Best Local Similarity
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Matches 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGPTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVY 1955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NQSCDIALLPENRGKORYNVILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08854585
Patent No. 6114140
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.1%; Score 1374; DB 1; Length 254; Best Local Similarity 99.2%; Pred. No. 8.9e-80; Matches 254; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
FILING DATE:
CLASSIFFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: JULY 25, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicaso
STATE: Illinois
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                                                                                                                                                   NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHQCVRDVLRARKLRS 1971
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                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                       254 amino acids
                                                                                                                                                                                                                                        TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 254 amino aci
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lir
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963 FHRLEAGEQYQIMIAS--VSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1308 PYNNRKSEGRIVYG-----LRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDK 1357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 SLTPGRLYTVTITTRSGKYENHSFSQE---RTVPDKV---QGVSVSNSARSDYLRVSWVH 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------TPEQGSNGTDGASQKTPSSTGPSPVFDIKAVSISPT----NVILTWKS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 ATGDFDHYEVTIKNKNNFIQTKSIPKSENB------CVFVQLVPGRLYSVTVTTKS 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 NDTAASEYKYVVKH------KMENEKTITVVHOPWCNITGLRPATSYVFSITPGI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTI----SGD--VQQSAFIE 902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     903 GFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVFEHT 962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              391 NESSSNYTYKIHVAGETDSSNLNVSEPRA------VIPGLRSSTFYNITVCPVLGDIE 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%; Score 1247; DB 2;
28.9%; Pred. No. 1.3e-70;
tive 215; Mismatches 547;
                                                                                                                                                                                                  27866/31954
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/237,940
                                                                                                                         NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFRENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 215;
                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHRACACTERISTICS: LENGTH: 1337 amino acids TYPE: amino acid
                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-854-585-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                  FILING DATE:
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963 FHRLEAGEQYQIMIAS--VSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA 1020
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142 NDTAASEYKYVVKH------KMENEKTITVVHQPWCNITGLRPATSYVFSITPGI 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 264;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 1337;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.9%; Score 1247; DB 2; Best Local Similarity 28.9%; Pred. No. 1.3e-70; Matches 417; Conservative 215; Mismatches 547;
                                                                                                   NAME: Rosenman Ph.D., Stephen J.
REGISTATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 200125.402C1
TELECOMMUNICATION INFORMATION:
                   APPLICATION NUMBER: US/09/447,533
FILING DATE: 23-NO. 6552169-1999
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-447-533-2
                                                                                                                                                                                 TELEPHONE: (206) 622-4900 TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      LENGTH: 1337 amino acids
                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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                                                                                                                    LLNIMMLVPHKRYLVSIKVQSAGMTSEVVEDSTITMIDRPPP--PPHIRVNEKDVLISK 1466
                                                                                                                                                                                                                                                                                     NY--FASKCAENPNSNSKS----FNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRIS 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         985 LVİ----VTVGGFIFWRKK---RKDAKNNEVSFSQIKP-------KKSKLİRVEN 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1688 FEGHFMKLQADSNYLLSKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPYDATRVKLS 1747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1628 FLIGMLVAVVALLICRQKVSHGRERPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKINQ 1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1748 NVDDDPCSDYINASYIPGNNFRREYIVTQGPLPGTKDDFWKMVWEQNVHNIVMVTQCVEK 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRILQQLDSK 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSVDIYGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLRARKLRS----EQENPLFPIYEN 1983
                                                                                                                                                 782 YLNF----STSYNISITTVSCGKMAAPTRNTCTTGITDPPPPDGSPNI----TSVSH 830
                                                                                                                                                                                                                                                                                                          881 TYVTYLIRTEEKGRSQSLSEVLKYEIDVGNESTTLG-----YYNGKLEPLGSYRAC 931
                                                                                                                                                                                                                                                                                                                                                                                                         932 VAGPTNITFHPONKGLIDGAESYVSPSR--YSDA-VSLP----ODPGVICGAVFGCIFGA 984
KAGNSSNATQVVTDIGITDATVTELIPGSSYTVELFAQVGDGIKSL-EPGRKSFCTDPAS 721
                                                                                                                                                                                                                              MASFDCEVVPKEPALVLKWTCPPGANAGFELEVSSGAWNNATHLESCSSENGTEYRTEVT
                                                                                                                                                                                                      SSINFTVNCSWFSDTNGAVKYFTVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group PLLC
STREET: Suite 6300, 701 Fifth Avenue
                                        IQNLHCR-PQNSTAIACSWIPPDSDFDGYSIE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHATASES
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Patent No. 6552169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 980104
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699
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Mon Mar 13

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27866/31954
               APPLICATION NUMBER: PCT/US95/05512 PILING DATE:
                                             ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27F
TELECOMMUNICATION INFORMATION:
                                                                                                                              TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              1337 amino acids
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSVDIYGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLRARKLRS----EQENPLFPIYEN 1983
                                                                                                                                            782 YLNF----STSYNISİTTVSCGKMAAPTRNTCTTGİTDPPPPDGSPNI-----TSVSH 830
663 KAGNSSNATQVVTDIGITDATVTELIPGSSYTVELFAQVGDGIKSL-EPGRKSFCTDPAS 721
                                                                               722 MASFDCEVVPKEPALVLKWTCPPGANAGFELEVSSGAWNNATHLESCSSENGTEYRTEVT 781
                                                                                                                                                                                                                                                                881 TYVTYLIRTEEKGRSQSLSEVLKYEIDVGNESTTLG------YYNGKLEPLGSYRAC 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application PC/TUS9505512 GENERAL INFORMATION:
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074 SKEAQTEGRTVPAAVTDLRITENSTRHLSFRWTASEGELSWYNIFLYNPDGNLQERAQVD 1133 1192 FNWSPASGDFDF-YELILYNPNGTKKENWKDKDLTEWRFQGLVPGRKYVLWV---VTHSG 1247 849 963 FHRLEAGEQYQIMIAS--VSGSLKNQINVVGRTVPASVQGVIADNAYSSYŞLIVSWQKAA 1020 1134 PLVQSFSFQNLLQGRMYKMVIVTH--SGELSNESFIFGRTVPASVSHLRGSNRNTTDSLW 1191 1308 PYNNRKSEGRIVYG------LRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDK 1357 391 NESSSNYTYKIHVAGETDSSNINVSEPRA-----VIPGIRSSTPYNITVCPVLGDIE 442 1248 DLSNKVTAESRTAPSPPSLMSFADIANTSLAITWKGPPDWTDYNDFELQWLPRDALTVFN 1307 GDPNSTAQYTR-----PSNVSNIDVSTNTTAATL----SWQNFDDASPTY---SYCLLIB 662 804 NDTAASEYKYVVKH------KMENEKTITVVHQPWCNITGLRPATSYVFSITPGI 190 191 G----NETWGDPRVİKVITEPIPVSDLRVAHGCBEGCSLSWSNGNGTASCRVLLESIGSH 246 EIQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTI-----SGD--VQQSAFIE 902 247 E--ELTQDSRL------QVNISDLKPGVQYNINPYLLQSNKTKGDPLAQKVAW-- 291 101 SLIPGRLYIVIIITIRSGKYENHSFSQE---RIVPDKV---QGVSVSNSARSDYLRVSWVH 754 97 499 TINOSIIIGGLFPGTKYCFEIVPKGPNGTEGASRTVCNRTVPSAVFDIHVVYVTTTE-MW 641 TVPSSVSGVTVNNSGRNDYLSVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFS 755 ATGDFDHYEVTIKNKNNFIQTKSIPKSENE------CVFVQLVPGRLYSVTVTTKS 903 GFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVFEHT 1021 GVAE---RYDILLLTENGILLRNTSEPATTKQHKFEDLTPGKK----YKIQILTVSGGLF 443 GTPGFLQVHTPPVPVSDFRVTVVSTTBIGLAWSSHDAESFQMHI---TQEGAGNSRVEI-50 TVATGENGITQISSTAESFHKQNGTGTP----QVETNTSEDG---ESSGANDSLR----Length 1337; GOYEANEQ-GNGRII-----PEPVKDLTLRNRSTEDLHVTWSGANG----Query Match
11.9%; Score 1247; DB 4; Length 1
Best Local Similarity 28.9%; Pred. No. 1.3e-70;
Matches 417; Conservative 215; Mismatches 547; Indels

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: 1711 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                             881 TYVTYLLIRTEEKGRSQSLSEVLKYEIDVGNESTTLG-----YYNGKLEPLGSYRAC 931
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TITLE OF INVENTION: PHOSPHATASE
1358 IQNLHCR-PQNSTAIACSWIPPDSDFDGYSIE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELIZABETH A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OLMSTED, BLIZABE
APPLICANT: MAURO, LAURA J.
APPLICANT: DAVIS, ALAN R.
APPLICANT: DIXON, JACK E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palo Alto
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STATE: C.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-342-930-2
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1038 LRNTSE-PATTKOHKFEDLTPGKKYKIQILTVSGGLFSKEAQTEGRTVPAAVTDLRITEN 1096
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PatentIn Release #1.0, Version #1.30
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              FLLING DATE: 21-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REPERENCE/DOCKET NUMBER: 20344-20975.00
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEEX: (415) 494-0792
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5	1157 HSGELSNESFTEGETVPASUSHIRGSNENTTDSIMENMSPASGDEDFVELILVNDNGTKK 1216	
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7	ENWXDKDLTEWRFQGLVPGRKYVLWVVTHSGDLSNKVTAESRTAPSPPSLMSFADIANTS	002
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Ħ	VKTVSGDSWKTYSKPIFGSVRTKPDKLQNLHCRPQNSTAIACSWIPPDSDFDGYS	ð
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7	1445 IDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVV 1492	ò
٠,	924 AEAWHPPELAEPPQVELGTGMGVTVMRGMFGKDDGQIQWYGIIATINMTLAQ 975	ପ୍ର
ř	1493READGSDELKPEQQHPLPSYLEYRH-NASIRVYQTNYFASKCAENPNSNSKSFNIKLG 1549	ò
٥,	976 PSREAINYTWYDHYYRGCESFLALLFPUNFYPEPWAGPRSWTVPVG 1021	셤
Ħ	1550 AEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKPLYSDTFF 1605	ò
1(1022 TEDCDNTQE-ICNGRLKSGFQYRFSVVAFSRLNTPETILAFSAFSEFRASISLA 1074	ପ୍
1(1606 SLPITTESEPLFGAIEGVSAGLFLIGMLVAVVALL-ICROKVSHGRERPSARLSIRRDRP 1664	ò
1,	1075 IIPLTVMLGAVVGSIVIVCAVLCLIRWRCLKGPRSEKDGFS-KELMP 1120	ପ୍ଧ
1(1665 LSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKEYEELKDVGRNQSCDIALL 1724	ò
11	1121 YNLWRTHRPIPIHSFRQSYBAKSAHAHQTFFQBFBBLKBVGKDQPRLEAEH 1171	đ
1.	1725 PENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGPLPGTKD 1784	δò
7	1172 PONIIKNRYPHVLPYDHSRVRLTQLPGEPHSDYINANFIPGYSHTQEIIATQGPLKKTLE 1231	q 0
1.	1785 DFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVLPEWTIR 1844	ð
1;	1232 DFWRLVWEQQVHVIIMLIVGMENGRVLCEHYWPANSTPVTHGHITIHLLAEEBEDEWTRR 1291	q _Q
18	1845 BFKI-CGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVH 1903	ò
1.	1292 EFQLQHGTEQKQRRVKQLQPTTWPDHSVPEAPSSLLAFVELVQEQVQATQGKGPILVH 1349	ପୁପ
Ħ.	1904 CSAGVGRIGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVYLHQC 1959	È
ï	1350 CSAGVGRTGTFVALLRILRQLEEEKVADVFNTVYILRLHRPLMIQTLSQYIFLHSCLINK 1409	අු
15	1960PRDVLRARKLRSEQENPLFPIYENVNPEYHR 1990	Š
'n	1410 ILEGPPDSSDSGPISVMDFAQACAKRAANANAGFLKEYKLLKQAIKDGTGSLLPPPDYNQ 1469	gg
ï	1991 DPVYSR 1996	ð
Ä	1470 NSIVSR 1475	음· ·
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Sequence 2, Application US/09822871
Patent No. 6723547
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,

RESULT 10 US-09-822-871-2

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1075 VPPAQPNGLVFYYVSL----ILQQTPRHVRPPLVTYERSIYFDNLEKYTDYILKITPST 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 YIAAETSAGT------GPKSNISVFTPPDVPGA------VFDLQLAEVEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 HDGESSLSBENDIFVRTSEDEPESSPQDVEVIDVTAD----EIRLKWSPPEKPNGIIIAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 NI-----TLSHKGTIKESRVLAPWITETHFKELVPGRLYQVTV-----SCVSGEL
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                                                                                                                                                                                                                                                                                                                                   lery Match 10.6%; Score 1107; DB 2; Length 2291;
set Local Similarity 23.8%; Pred. No. 2.5e-61;
ttches 519; Conservative 324; Mismatches 790; Indels 550;
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1219
CURRENT APPLICATION NUMBER: US/09/822,871
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2291
TYPE: PRT
ORGANISM: Human
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RESULT 11
US-09-822-871-4
; Sequence 4, Application US/0982871
; Patent No. 6723547
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; TITLE OF INVENTION: AND USES THEREOF
; TITLE OF SEPERATE SEPERATION NUMBER: US/09/822,871
; CURRENT APPLICATION NUMBER: US/09/822,871
; CURRENT PILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
                                                                                                                                                                     OFVRIVRDYINRSPGAGPTVVHCSAGVGRIGIFIALDRILQQLDSKDSVDIYGAVHDLRL 1941
QEEFSELPKFLQDLSSTDADLPWNRAKNRFPNIKPYNNNNRVKLJADASVPGSDYINASY 2054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNIAITAVS----GGKRSFSVYTNGSTVPSPVKDIGIS-TKANSLLISW---SHGSGNVE 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 OYRVKVSVLETGVVLENTLLTGODESISNPMSPEIMNLVDPMIGFYEGSGEMSSDLHSPA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 PTFRIDNTTYGCNLQDLQAGTIYNFKIISLDEE-----RTVVLQTDPLP--PARFGVSKE 121
                                                                                                           I PGNNFRREYI VTQGPLPGTKDDFWKMVWEQNVHNI VMVTQCVEKGRVKCDHYWPADQDS
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                                                         2055 ISGYLCPNEFIATOGPLPGTVGDFWRMVWETRAKTLVMLTQCPEKGRIRCHQYWPEDNKP
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Best Local Similarity
Matches 545; Conserva
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ORGANISM: Rat
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| : :: | | | | | | : :| | 1.130 EKGFSDTYTAQLYIKTEEDVPETSPIINTFKNLSSTSVLLSSWDPPVKPNGAIISYDLTLQ 1189
                                                              984 KNOINVVGRTVPASVOGVIADNAYS---SYSLIVSW---OKAAGVAERYDILLITENGIL 1037
                                                                                                                                                                                                                                                                                                               1038 LRNTSEPATTKOHKFEDLTPGKKYKIQILTVSGGLFSKEAQTEGRTVPAAVTDLRITENS 1097
                                                                                                                                                                                                                                                                                                                                                                                     ---TTOLRAQKCKEWESEECVEYQKIQYL--------YEAHLTET 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------YRFQ-----VAAST 1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | : : | : | | : | | 1576 KSVDNDEFNISFIKSNBENK-TIEIKDLEIF-----TRYSVVITAFTGNISAAYVBG 1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1704 SKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPY-DATRVKLSNVDDDPCSDYINASY 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SGDFDFYELILYNPNGTKKENWKDKDLTEWRFOGLVPGRKYVLWVVTHSGDLS----N 1251
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                                                                                                         IP-EPVKDLTLRNRSTEDLHVTWSGA---NGDVDQYEIQLLFNDMKVFPFFHLVNTATEY 873
                                                                                                                                                                     874 RFTSLTPGRQYKILV--LTISGDVQQSAFIEGFT----VPSAVKNIHISPNGATDSLTVN 927
                                                                                                                                                                                                                                  WTP---GGGDVDSYTVSAFRHSQKVDSQTIPKHVFEHTFHRLEAGEQYQIMI-ASVSGSL 983
                                                                                                                                                                                                                                                   1360 WDPPKKANGIIIQYMVTVERNSTKVSPQ---DHMY--TFIKLLANTSYVKKVRASTSAGE
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                                            NKNNFIQTKSIPKSENECVFVQLVPGRLYSVTVTTKSGQYEANEQGNG-
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604 TIYATELDTNRAFQMTTVDNSFLITGLKKYTRYKMRVAASTHVGESSLSEENDIFVRTPE 663	394	VMDDTGLVPGRQYEVEVIVESGNLKNSERCQGRTVPLAVLQLRVKHANETSLSIMWQT		490 PVAEWEKYIISLADRDLLLIHKSLSKDAKEFTFTDLVPGRKYMATVTSISGDLKNSSSVK 549	GRTVPAQVTDLHVANQGMTSSLFTNWTQAQGDVEFYQVLLIHENVVIKNESISSETSRYS	:	610 FHSLKSGSLYSVVVTTVSG-GISSRQV-VVEGRTVPSSVSGVTVNNSGRND 658	830EVSASTLKGEGIRSRPISILTEEDAPDSPPQNFSVKQLSGVTV 872	659 YLSVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTI 712	713 TTRSGKYENHŞFSQERTVPDKVQGVSVŞNSARSDYLRVSWVHATGDFDH 761	: : : : : : : : : : : : :	YEVTIKNKNVTVTTKSGOYEANE	YSVYYQNTSGTFVQNFTLLQVTKESDNVTVSARIYRLAIFSYYTFWLTASTSVGNGNK	812 QGNGRIIPB-PUXDLTLRNRSTEDIHUTWSGANGDVDQYEIQLLFNDWKVF 861 STATEMENT	862 PPFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEGFTVP 907	1097 PPRHMIPPLVTYENSIDFDDLEKYTDY-IFKITPSTEKGFSETYTTQLHIKTEEDVP 1152	908 SAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVFEHTFH 964	RLEAGEGYQIMIASVSGSLKNQINVVGRTVPASVQGVIADNAY	1200 -VISGNHIVLEELSPFTLYSFFAAARTWKGLGPSSILFFYTDESAPLAPPQNLTLINY 1256	1008 SSYSLIVSWQKAAGVAERYDILLITENGILLRNTSEPATTKQHKFEDLTPGKKYK 1062 	IQILTVSGCLFSKEAQ-TEGRTVPAAVTDLRITENSTRHLSFRWTASEGELSW	VSVSAFTKVGNGNQXSNVVEFTTQESVFEAVRNIECVARDMQSVSVRWDFPRKFINGILIH	1115 YNIELYNPDGANLOGERAQVDELVQSFRONLLGGRAYKAV1VTHSGELESSFIF 1168 1375 YMITVGGNSTKVSPRDPTYTFTKLLPNTSYVFEVRASTSAGE-GNESRCDISTL 1427	1169 GRTVPASVSHLRGSNRNTTDSLWFNWSPASGDFDFYELILYNPNGTKKKNW 1219	1428 PETVPSAPTNVAFSNVQST-SATLTWTKPDTIFGYFQNYKITTQLRAQKCREWEPBECIE 1486		1487 HQKDQYLYEANQTEETVHGLKKFRWYRFQVAASTNVGYSNASEWISTQTLPGPPDGPPEN 1546	1270 ADIANTSLAITWKGPPDWTDYNDFELQWLPRDALTVFNPYNNRKS 1314 124
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                   1589 DEDLKEFTKPLYSDTFFSLPITTESEPLF-GAIEGV-SAGLFLIGMLV---AVVALLICR 1643
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EGRIVYGLRPGRSYQFNVKTVSGDSWKTYSK------PIFGSVRTKPDKIQNLHCRP 1365
                                                           1366 QNSTAIACSWIPPDSDFDG----YSIECRKMDTQEVE---FSRKLEKEKSLLNIMM-LV 1416
                                                                                                                        1417 PHKRYLVSI-KVQSAGMTSEVVEDSTITM----IDRPPPPPPHIRVNEKDVLISKSSINF 1471
                                                                                                                                                                                     1472 IVNCSWFSDTNGAVKYFTVVVREADGSDELKPEQOHPLPSYLEYRHNASIRVYOTN--YF 1529
                                                                                                                                                                                                                                                    1530 ASKCAENPNSNSKSFNI-KLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLF 1588
                                                                                                                                                                                                                                                                                                                                                                                1644 QKVSHG-----RERPSARLSIRRDRPLSV-HINLGQK-----GNRKTSCPIKINQFEGH 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                               1692 FWKLQADSNYLLSKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPYDATRVKLSNVDD 1751
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC Compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: WENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT PAPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/21,755
PRIOR APPLICATION NUMBER: 60/21,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-00-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASELSEQ FOR WINDOWS Version 4.0
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                           1251 NKVTAESRTAPSPPSLMSFADIANTSLAITWKGPPDWTDYNDFE-LQWLPRDALTVFNPY 1309
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                                                                                                         1310 NNRKSEGRIVYGLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRT----KPDKIQNLHCR 1364
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----ERGSNTSMLRLVKL-
                                                   749 ADFFEVFCQQVGSSQKTKLQEPVAVSS-----HVVTI-----
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                                                                                                                                                                                                                                    ----SVTACT----
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8.7%; Score 915.5; DB 1;
Best Local Similarity 24.0%; Pred. No. 1.5e-49;
Matches 367; Conservative 200; Mismatches 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 LFTNWTQAQGDVEFYQVLLIHENVVIKNES-----
    US/08/201,697
    ATTORNEY DATE: 25-FBB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryb A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-901

TELEPAX: (619) 635-8949

INPORMATION FOR ESQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 1188 amino acids

LENGTH: 1188 amino acids
                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-201-697-4
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                   Gaps
                                                                                                                                                 Indels 481;
                                                                                                                                                                                        ---ISSETSRY---
                                                                                                               Length 1246;
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                                                                                                             Query Match
8.7%; Score 913.5; DB 2;
Best Local Similarity 24.0%; Pred. No. 2.1e-49;
Matches 367; Conservative 199; Mismatches 483;
                                                                                                                                                                                      571 LFTNWTQAQGDVEFYQVLLIHENVVIKNES---
; SEQ ID NO 8051
; LENGTH: 1246
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8051
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& 8 &	IKVQSAGMTSEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGA
a & a	807 ADFFEVFCQQVGSSQKTKLQEPVAVSSHVVTI
දු පු	1605 FSL-PITTESEPLFGAIEGYS-AGLFLIGMLVAVVALLICRQK-VSHGRERPSARL 1657 :::
ò a	1658 SIRRDRPLSVHLNLGQKGNRXTSCPIKINQFEGHFMKLQADSNYLLSKBYBELKDVGRNQ 1717
& 8	1718 SCDIALLPENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQG 1777
& 48	1778 PLPGTKDDFWKKNYWEQNYHNIVMVTQCVEKGRYKCDHYWPADQDSLYYGDLILQMLSESV 1837
& a	1838 LPEWTIREFKICGEEQLDAHRLIRHFHYTVWPDHGVPETTGSLIQFVRTVRDYINRSP 1895
ò a	1896 GAGPTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVY 1955 ::
දු පු	1956 LHQCVRDVLRARKLRSEQENPLFPIYENVN 1985 : :
RESULT 1. US-09-946 ; Sequent; ; Patent ; GENERAL ; TITLE ; TITLE ; TITLE ; TITLE ; TITLE ; FILE PRIOR ; SOFTW	14 949-016-8052 ence 8052, Application US/09949016 ence 8052, Application US/09949016 ent No. 6812339 RAL INFORMATION: LICANT: VENTER, J. Craig et al. LICANT: VENTER, J. Craig et al. LICANT: VENTER, J. Craig et al. LE OF INVENTION: WITH HUMAN DISEASE, METHODS OP DETECTION ENTERT FILING DATE: 2000-04-14 RENT FILING DATE: 2000-10-20 OR FILING DATE: 2000-10-20 OR FILING DATE: 2000-10-3 OR FILING DATE: 2000-10-3 OR FILING DATE: 2000-09-08 BRE OF SEQ ID NOS: 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012 TWARE: PREUSER 207012
Query Best Match	ry Match L Local Similarity 24.0%; Pred. No. 2.1e-49; ches 367; Conservative 199; Mismatches 483; Indels 481; Gaps 63;
ò	571 LFTNWTQAQGDVEFYQVLLIHENVVIKNESISSETSRY 608

Qy 1605 FSL-PITTESEPLFGAIEGUS-AGLFLIGMLVAVVALLICRQ	RESULT 15 US-09-49-016 Sequence 8053, Application US/09949016 Patent No. 681239 Sequence 8053, Application US/09949016 Patent No. 681239 GENERAL INFORMATION: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DISTINCE APPLICATION NUMBER: US/09/1949,016 CURRENT PILING DATE: 2000-04-14 PRIOR PRILING DATE: 2000-06-04-14 PRIOR PRILING DATE: 2000-09-08 PRIOR PELING DATE: 2000-09-08 PRIOR FILING DATE: 2000-09-09 PRIOR FILING DATE: 2000-09 PRIOR FILING DATE: 2000-09 PRIOR FILING DAT
81 LFKNATAFHVTVQDDNNIVVSLEASDVISPASVYVVKITGESKNYFFEFEEFNS 134 609SFHSLKSGSLYSVVYTTVSGGISGRQVVVBGRTVPSSVSGYTVNNSG 655 135 TLPPPVIFKASYHGLYYIITLVVVNGNVYTKPSRSITYLTRPLPVTSVSIYDYK 188 656 RNDYLSVSWLVAPGDVDNYEVTLSH-DGKVVQSLVIAKSVRECSFSSLTPGKL 707 189 PSPETGVLETHYPEKYNVFTRVNISYMEGKDPRTWLTKTDFFKGTVFNHMLPGMC 244 708 YTVTITRSGKYENHSFSQERTVPDFKYGVSVSNSARSDYLRV 750	SEE PRHYPEHTERAGEOYOIMIAGNOSIKNOINVVGRTVPASVOGVIADNAYSSYSIIV 1014
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DETECTION AND USES THEREOF DSNYLLSKEYEELKDVGRNQ 1717 ||:| | ::|||| :| DSDYKFSLQFEELKLIGLDI 982 ADQDSLYYGDLILQMLSESV 1837
:::|||:::|||
FTEEPLAYGDITVEMISEEE 1102 VHDLRLHRVHMVQTECQXVY 1955 | ::| :| :| || || || : VSEMRSYRMSMVQTEEQXIF 1217 NOK-VSHGRERPSARL---- 1657 Indels 481; Gaps 63; |:| : || : RKKHLQMARECGAGTFVNFA 922 VVEGRTVPSSVSGVTVNNSG 655 VOGVSVSNSARSDYLRV--- 750 | :|| | | Length 1246;

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293	803	345	855	895	460	954	493	1014	530	1074	1130	636	1190	629	1250	619	1309		1364	1424	119	1484		838	1604	864	1657	922	1717	1777	1042
YSNITFQLVSEATFNKSTLVEXSGVSHEPKQHRTAPYPPQNISVRIVNL	SWVHATGDFDHYEVTIKNKNNFIQTKSIPKSBNBCVFVQLVPGRLYS	: : : : : :	SGOYEANEOGNGRIIPEPVKDLILRNRSTEDLHVTWSGANGDVDQYEIQLLF		TWLPPKPPTAFDGFH-IHIEREENFTEYLMVDBEAHEFVA		-SSGSCETRKSQSAKSLSFYISPSGEWIEELTEK	PKHVFEHTFHRLEAGEQY	POHVSVHVLSSTTAVSVVSLTC	SWQKAAGVAERYDILLLTENGILLENTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFS	KEAO-TEGETUDANUTUTA TUTUTA TEGETUTA		QVDPLVQSFSFQNLLQGRMYK	: : : : : : TYYEIAATUSLTASVRIANLLPA	WFNWSPASGDFDFYELI	WYYNFRVI-MVIWGDPELSCC	NKVTAESRTAPSPPSIMSFADIANTSLAITWKGPPDWTDYNDFE-LOWI-PRDALTVFNPY :		NNRKSEGRIVIGERFORKSTOFNVKTVSGDSWKITSKFIFGSVKIKPOKIONHCK : :	PQNSTAIACSWIPPDSDFDGYSIECRKMDTQEVEFSRKLEKEKEKEKLINIMMLVPHKRYLVS : :	SVTACTERGSNTSMIRLUKL	IKVQSAGMTSEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDT	VKYFTVVVPRANGSDRIKEPROHPI BSVI EVPHNASTRVOTIVFA		NIKLGAEMESLGGKRDPTQQKFC				SIRRDRPLSVHLNLGQKGNRKTSCPIKINQPEGHFMKLQADSNYLLSKEYEELKDVGRNQ : : : : : :	SCDIALLPERRGKNRYNNILPYDATRUKLSNUDDDPCSDXINASYIPGNNFRREYIUTQG 1777	
245	751	294	804	95.0	406	968	461	955	494	1015	1075	577	1131	637	1191	99	1251		1310	1365	760	1425	1485	807	1545	839	1605	865	1658	1718	983
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1778 PLPGTKDDFWKRVWEGNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESV 1837	1838 LPEWTIREFKICGEEQLDAHRLIRHFHYTWNPDHGVPETTQSLIQFVRTVRDYINRSP 1895 1103 QDDWACRHFRINYADEMQDVMHFNYTAWPDHGVPTANAAESILQFVHMVRQQATKS- 1158	1896 GAGPTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVX 1955 	1956 LHQCVRDVLRARKLRSEQENPLFPIYENVN 1985 : : : : : 1218 IHQCVQLMMMKKKQQFCISDVIYENVS 1244
1778	1838	1896	1956
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Search completed: March 10, 2006, 18:39:37 Job time : 62.7221 secs

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10483
1 MLSHGAGLALWITLSLLQTG......FPIYENVNPEYHRDPVYSRH 1997
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1. /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2. /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ajo			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	10483	100.0	1997	4	US-10-634-027-2	Sequence 2, Appli
7	10480	99.9	1997	'n	US-10-756-149-5168	51
ю	10460	8.66	1997	ო	US-09-909-567B-54	Sequence 54, Appl
4	10460	93.8	1997	4	US-10-408-765A-2135	
Ŋ	10460	99.8	1997	Ŋ	US-10-497-692-4	Sequence 4, Appli
9	7614	72.6	1450	ഗ	US-10-497-692-14	Sequence 14, Appl
7	1830	17.5	336	4	US-10-634-027-4	Sequence 4, Appli
8	1691	16.1	319	4	US-10-634-027-7	Sequence 7, Appli
6	1690	16.1	312	4	US-10-634-027-6	Sequence 6, Appli
10	1556.5	14.8	1647	Y	US-11-097-143-2076	
11	1485.5	14.2	1767	4	US-10-087-684-40	
12	1485.5	14.2	1767	4	US-10-218-779-40	4
13	1485.5	14.2	1767	9	US-11-097-143-14970	
14	1475.5	14.1	1767	4	US-10-087-684-41	4.
15	1475.5	14.1	1767	4	US-10-218-779-41	41,
16	1433.5	13.7	1447	ß	US-10-497-692-13	13,
17	1374	13.1	310	m	US-09-788-626-15	15,
18	1247	11.9	1337	4	US-10-390-501-2	ď
19	1243.5	11.9	1238	4	US-10-366-547-47	47,
20	1242	11.8	1337	4	-366-547	42,
21	1242		1337	4	US-10-723-606-2	ď
22	1221.5		1216	4	US-10-366-547-49	49,
23	1206		1337	4	US-10-366-547-44	44,
24	1204		1705	ហ	US-10-029-345A-37	37,
25	1198		1711	ഹ	US-10-029-345A-38	38,
26	1107		2291	'n	-09	ď
27	1107		2291	4	US-10-673-885-2	ď

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Sequence 6, Appl	Sequence 6, Appli	Sequence 10, App.	Sequence 10, Appl	Seguence 2, Appl	Sequence 4, Appl	Seguence 4, Appl	Sequence 37, App]	Sequence 37, App.	Seguence 5508, A	Sequence 5509, A	Sequence 79, App	Sequence 34, Appl	Sequence 27, App.	Sequence 3, Appli	Sequence 4, Appli	7	8
US-10-087-684-6	US-10-218-779-6	US-10-087-684-10	US-10-218-779-10	US-10-466-759-2	US-09-822-871-4	US-10-673-885-4	US-10-087-684-37	US-10-218-779-37	US-10-369-493-5508	US-10-369-493-5509	US-10-331-496A-79	US-10-789-241-34	US-10-029-345A-27	US-10-723-606-3	US-10-245-539-4	US-10-245-539-2	US-10-245-539-8
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2281	2281	2300	2300	2299	2301	2301	2302	2302	1367	1367	1188	1188	1188	341	1093	1118	1118
10.6	10.6	10.5	10.5	10.5	10.5	10.5	10.5	10.5	9.0	9.0	8.7	8.7	8.7	8.5	8.5	8.5	8.5
1106	1106	1100.5	1100.5	1099.5	1097	1097	1097	1097	939	939	913.5	913.5	913.5	889.5	886	886	988
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ALIGNMENTS

RESULT 1

361 VSGELSAQKMAVGRTFPDKVANLEANNNGRWRSLVVSWSPPAGDWEQYRILLFNDSVVLL 420 	
421 NITVGKETQVVMDDTGLVFGRQYEVEVIVESGNLKNSERCQGRTVPLAVLQLRVKHANE 480	1501 LKPEQQHPLPSYLEYRHNASIRVYQTNYFASKCAENPNSNSKSFNIKLGAEMESLGGKRD
81 TSLSIMWQTPVAEWEKYIISLADRDLLLIHKSLSKDAKEFTFTDLVPGRKYMATVTSISG	Qy 1561 PTQQKFCDGPLKPHTAYRISIRAFTQLFDBDLKEFTKPLYSDTFFSLPITTESEPLFGAI 1620
41 DLKNSSSVKGRTVPAQVTDLHVANQGMTSSLFTNWTQAQGDVEFYQVLLIHENVVIKNES	QY 1621 EGYSAGLFLIGMLVAVVALLICRQXVSHGRERPSARLSIRRDRPLSVHLNLGQKGNRKTS 1680
ISSETSRYSFHSLKSGSLYSVV7TVSGG1SSRQVVVEGRTVPSSVSGYTVNNSGRNDYL	Qy 1681 CPIKINQFEGHFWKLQADSNYLLSKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPYD 1740 Db 1681 CPIKINQFEGHFWKLQADSNYLLSKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPYD 1740
SVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSGFSSLTPGRLYTVTITTRSGKYE	Qy 1741 ATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTGGPLPGFKDDFWRAVWEGNVHNIVM 1800 Db 1741 ATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTGGPLPGTKDDFWRAVWEGNVHNIVM 1800
NHSFSQERTVPDKVQGVSVSNSARSDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIPK	QY 1801 VTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVLPEWTIREFKICGEEQLDAHRLI 1860 DD 1801 VTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVLPEWTIREFKICGEEQLDAHRLI 1860
SENECVEVOLVEGRIXSUTVITYGGOYBANEQGNGRIT PEPVKDI.TLRNRSTEDLHVIWS	OY 1861 RHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRI 1920 1861 RHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRI 1920
GANGDVDQYEIQLENDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAF	Oy 1921 LQQLDSKDSVDIYGAVHDLRLHRVHAVQTECQYVYLHQCYRDVLRARKLRSEQENPLFPI 1980 Db 1921 LQQLDSKDSVDIYGAVHDLRLHRVHAVQTECQYVYLHQCVRDVLRARKLRSEQENPLFPI 1980
	Qy 1981 YENVNPEYHRDPVSRH 1997 Db 1981 YENVNPEYHRDPVSRH 1997
961 HTFHRLEAGEGYGIMIASVSGSLKNOINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA 1020 	RESULT 2 US-10-756-149-5168 ; Sequence 5169, Application US/10756149
1021 GVAERYDILLITENGILLRNTSEPATTKQHKREDLTPGKKYKIQILTVSGGLFSKEAQTE 1080 	
1081 GRTVPAAVTDLRITENSTRHLSFRWTASEGELSWYNIFLYNPDGNLQERAQVDPLVQSFS 1140 	TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND FILE REPERENCE: INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER; FILE REPERENCE: file (CIRRENT APPLICATION NUMBER: US,10,756,149)
1141 FQNLLQGRMYKMVIVTHSGELSNESFIFGRTVPASVSHLRGSNRNTTDSLWFNWSPASGD 1200 	; CURKENI FILING DAIE: 0.04-01-12; NUMBER OF SEQ ID NOS: 5818; SOFTWARE: Patentin version 3.2;
1201 FDFYELILYNPNGTKKENWKDKDLJEWRFQGLVPGRKYVLWVYTHSGDLSNKYTAESRTA 1260 	; TYPE: PTT ; TYPE: PTT ; ORGANISM: Homo Sapiens US-10-756-149-5168
1261 PSPPSLMSFADIANTSLAITWKGPPDWTDYNDFELGMLPRDALTVFNPYNRKSEGRIVY 1320 	Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 1996; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1321 GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTAIACSWIPPDS 1380 	OY 1 MLSHGAGLALMITLSLLOTGLAEPERCNFTLAESKASSHSVSIOWRILGSPCNFSLIYSS 60
1381 DFDGYSIECRKMDTOEVEESRKLEKEKSLLNIMMLVPHKRYLVSIKVQSAGWTSEVVEDS 1440 	OY 61 DTLGAALCPTFRIDNTTYGCNLQDLQAGTIYNFKIISLDEERTVVLQTDBLPPARFGVSK 120
1441 TITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVREADGSDE 1500	Qy 121 EKTTSTGLHVWWTPSSGKVTSYEVQLFDENNQKIQGVQIQESTSWNEYTFFNLTAGSKYN 180

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1020
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                         SVSWLLAPGDVDNYEVTLSHDGKVVOSLVIAKSVRECSFSSLTPGRLYTVTITTRSGKYE 720
                                                                                         GANGDVDQYEIQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAF
                                                                                                                                                                                                                                                                                                                                                              IEGFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTFHRLEAGEGYOIMIASVSGSLKNOINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1321 GLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNSTAIACSWIPPDS
                                                                                                                                                                               SENECVFVQLVPGRLYSVTVTTKSGQYEANEQGNGRTIPEPVKDLTLRNRSTEDLHVTWS
                                                                                                                                                                                                                                                                                                                                    IEGFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSPPSLMSFADIANTSLAITWKGPPDWTDYNDFELQWLPRDALTVFNPYNNRKSEGRIVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFDGYSIECRKMDTQEVEFSRKLEKEKSLLNIMMLVPHKRYLVSIKVQSAGMTSEVVEDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FONLLOGRMYKMVIVTHSGELSNESFIFGRTVPASVSHLRGSNRNTTDSLWFNWSPASGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTQQKPCDGPLKPHTAYRISIRAFTQLFDBDLKBFTKPLYSDTFFSLPITTESBPLFGAI
                                                                                                                                                          SENECVFVQLVPGRLYSVTVTTKSGQYEANEQGNGRT1PEPVKDLTLRNRSTEDLHVTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDFYEL1LYNPNGTKKENWKDKDLTEWRFQGLVPGRKYVLWVVTHSGDLSNKVTAESRTA
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| Publication No. US20040101874A1
| Sequence 2135, Application US/10408765A
| Publication No. US20040101874A1
| SERRAL INFORMATION:
| APPLICANT: Ghang, Bing
| APPLICANT: Zhang, Bing
| APPLICANT: Taylor, Steven W.
| APPLICANT: Taylor, Steven W.
| APPLICANT: Glenn, Gary M.
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                                                Length 1450;
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                                              Query Match
72.6%; Score 7614; DB 5;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1448; Conservative 1; Mismatches 1;
; LENGTH: 1450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-692-14
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                                                TITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVREADGSDE 1500
                                                         DFDGYSIECRKMDTQEVEFSRKLEKEKSLLNIMMLVPHKRYLVSIKVQSAGMTSEVVEDS
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   121 TKDDFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVLPEW 180
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                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10634027

| Sequence 7, Application US/10634027
| Publication No. US20040077065A1
| GENERAL INFORMATION:
| APPLICANT: Procter & Gamble Company
| APPLICANT: Procters Matthew E
| TILLE OF INVENTION: Three Dimensional Coordinates of HPTPbeta
| TILLE OF INVENTION: Three Dimensional Coordinates of HPTPbeta
| TILLE OF INVENTION NUMBER: US/10/634,027
| CURRENT FILING DATE: 2003-09-04
| PRIOR FILING DATE: 2003-09-05
| NUMBER OF SEQ ID NOS: 15
| SOFTWARE: Patentin version 3.2
| TENGIN 1005 70
| TENGIN 1005 70
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10S-10-634-027-6
Sequence 6, Application US/10634027; Publication No. US20040077065A1
GENERAL INFORMATION 6: APPLICANT: Procter & Gamble Company; APPLICANT: Evodokimov, Artem G
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Matches 312; Conserv
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                                                                                                SNSKSFNIKLGAEMESLGGKCDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKP 1080
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 SDTNGAVKYFTVVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQTNYFASKCAENPN 1538
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| Publication No. US20040077065A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Prodess, Matchew B
| APPLICANT: Pokross, Matchew B
| TITLE OF INVENTION: Three Dimensional Coordinates of HPTPbeta FILE REFERENCE: 9049A2
| CURRENT PILING DATE: 2003-08-04
| FRIOR APPLICATION NUMBER: US 60/413,547
| FRIOR APPLICATION NUMBER: US 60/413,547
| RIOR FILING DATE: 2002-09-25
| NUMBER OF SEQ ID NOS: 15
| SCPTWARE: Patentin version 3.2
| SEQ ID NO 4
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100.0%; Pred. No. 2e-108;
tive 0; Mismatches 0;
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                               ------MATVTSISGDLKNSSSVKGRTVPAQVTDLH
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                                                                                                                                                                             Length 1647;
                                                                                                                                                                                                                     209;
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                                                                                                                                                                          Query Match

14.8%; Score 1556.5; DB 6;
Best Local Similarity 30.3%; Pred. No. 6.7e-90;
Matches .474; Conservative 254; Mismatches 627;
                                                                                                                                                                                                                                                                                         | |: :|| || EIQFSRALPGTKYNFWLYYTNFTHHDWLTWTVTIT----
    NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2076
LENGTH: 1647
TYPE: PRT
ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                               519 EFTFIDLVPGRKY------
                                                                                                                                   US-11-097-143-2076
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TITLE OF INVENTION: DREECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOOO728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 1999-10-12
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APPLICANT: Pokross, Matthew E
TITLE OF INVENTION: Three Dimensional Coordinates of HPTPbeta
FILE REPERENCE: 9045M2.
CURRENT APPLICATION NUMBER: US/10/634,027
CURRENT FILING DATE: 2003-08-04
PRIOR PLILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 312
                                                                                                                                                                                                                                                                                                                             Length 312;
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                                                                                                                                                                                                                                                                                                                         Ouery Match
16.1%; Score 1690; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.6e-99;
Matches 312; Conservative 0; Mismatches 0;
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Publication No. US20050208558A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/184,831
FILING DATE: 2000-02-24
APPLICATION NUMBER: 60/191,637
FILING DATE: 2000-03-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVLRARKLRSEQ 312
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-10-634-027-6
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APPLICANT: Malyankar, Uriel M.
APPLICANT: Guo, Xiaojia
APPLICANT: Guo, Xiaojia
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-214 CIP
CURRENT APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-30
PRIOR PLINIG DATE: 2000-11-30
PRIOR PLINIG DATE: 2000-11-36
PRIOR FILING DATE: 2001-01-25
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                            PIL---APPRPATOVVPTEVYRSSTIQIRFRKNYFSDQNGQVRMYTIIVAE----DDAK 1119
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DB 4; Length 1767;
                                                           197;
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Query Match
14.2%; Score 1485.5; DB 4;
Best Local Similarity 29.2%; Pred. No. 2.6e-85;
Matches 475; Conservative 269; Mismatches 687;
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Padigaru, Muralidhara

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Mishra, Vishnu Shenoy, Suresh G.

Ratelli, Luca Tchernev, Velizar T. Vernet, Corine A.M. Zerhusen, Bryan D.

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                                                         EDLIPGKKYKIQILIVSGGLFSKEAQTEGRIVPAAVIDLRITENSTRHLSFRWIASEGEL 1112
                                                                                                                                        1113 SWYNIFLYNPDGNLQERAQVDPLVQ-----SFSFQNLLQGRMYKM-VIVTHSGELS 1162
                                                                                                                                                                                                                                                                                                   1212 NGTKKENWKDKDLTEWRFQGLVPGRKYVLWVVTHSGDLSN-KVTAESRTAPSPPSLMSFA 1270
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1241 VYSSPITTERSDTVIVAATVSA-VLLVAMVLVVV---YCQHRCQ--LIRRASKLARMQDE 1294
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102 PNTTIPASDIGKDIK---FSRALPGTEYNFWLYYTNSTHREQLTWTVNITTAPDPPANLS 158
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APPLICANT: Miller, Charles
APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT APPLICATION NUMBER: 60/253,834
PRIOR APPLICATION NUMBER: 60/255,834
PRIOR PILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-130
PRIOR FILING DATE: 2001-13-0
PRIOR PRILING DATE: 2001-13-0
PRIOR PELING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
Sequence 40, Application US/10218779
Publication No. US20040029222A1
GENERAL INFORMATION:
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Mishra, Vishnu
Patturajan, Meera
Shenoy, Suresh
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ORGANISM: Drosophila melanogaster
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Grosse, William
Alsobrook II, John
Lepley, Denise
Rieger, Daniel
Burgess, Carherine
Casman, Stacie
Spytek, Kimberly
                                                                                                        MacDougall, John
Millet, Isabelle
Ellerman, Karen
Stone, David
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Tchernev, Velizar
Vernet, Corine
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Malyankar, Uriel
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Boldog, Ferenc
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APPLICANT: Venter, J. Craig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1271 DIANTSLAITWKGPPDWTDYNDFELQWLPRDALTVFNPYNNRKSEGRIVYGLRPGRSYQF 1330
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               GDSVYFDYPDILEPGRIYEVVVKIIADNVNSWPASGEVTLRPRPVRSLGGFLDDRSNA-L 451
                                                                                                                                                                             887 LVLTISGDVQQSAF-IEGFTVPSA--VKNIHISPNGATDSLTVNWTPGGGDV----DSYT 939
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TLSHDGKVVQSLVIAK----SVRECSFSSLTPGRLYTVTITTRSGKYENHSFS----Q 726
                                                   ERTVPDKVQGVSVSNS-ARSDYLRVSW--VHATGDFDHYEVTIKNKNNPIQTKSIPKSEN 783
                                                                                                         -ECVFVQ----LVPGRLYSVTVTTKSGQYEANEQGNGRTI-PEPVKDL--TLRNRSTEDL 835
                                                                                                                                                             HVTWSGA-NGDVDQYEIQL--LFNDMKVFPPF-----HLVNTATEYRFTSLTPGRQYKI 886
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LPENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGPLPGTK 1783
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                                                                                                                                                                                                                                                                                                                        1844 REFKI----CGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPT 1900
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EXPRESSION OF 10,000 OR
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCI
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCI
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOO0728
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-11-2
PRIOR PELLON DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PELLON DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PELLON DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PELLON DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR PELLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFUTH NO 14970
LENGTH: 1767
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61	218 Qy 1604 676	278 Db 1241	72	R 335 Qy 1724 LPE	392 Db 1350	Oy 1784 DDE 11	451 Ov 1844	886 ST 131	. 939 Qy 1901	E 564 Db 1522 IVF	998 Db 1582 623	1052 RE	675) GENERAL INFOR PELICANT: 5 735 ; APPLICANT: 7	S 1162 ; APPLICANT: MI ; APPLICANT: E1 ; APPLICANT: St	793 ; APPLICANT:	1211 ; APPLICANT: ; APPLICANT: ; APPLICANT:) APPLICANT: ; APPLICANT: ; APPLICANT:	606	1330 ; APPLICANT: ; APPLICANT:	F 96/ ; AFFLICANI: 1C ; APPLICANI: Ve W 1375 ; APPLICANI: Ze	; APPLICANT:	1430	1087 ; FILE REF	1490 ; CURREN	FRIOR APPLICATE PRIOR FILING DE 1544
	159 VQLKSSKSAFINKFEGSKKIGGFKIKVLGALIDLFFEKSISLEGNEILGLSAKELIFGGS 619 YSVVVTTVSGGISSRQVVVEGRTVPSSVSGVTVNNSGRNDYLSVSWLVAPGDVDNYEV		TLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVIITTRGGKYENHSFS	279 SITPDDAIGSVLYVEREGEPFGPAARKGLVPGREKNISVQTVSEDEISSVPTTAR 727 ERTUDDKUNGVSVSNS-EDRONIBUGGVHATGDEDHVEVTTRAKANDFINTKSEEDE		784 -ECVFVQLVPGRLYSVTVTTKSGQYEANEQGNGRII-PEBVKDLTLRNRSTEDL : :	393 GDSVYFDYPDILEPGRIYEVVVKTIADNVNSWPASGEVTLRPRPVRSLGGFLDDRSNA-L	836 HVTWSGA-NGDVDQYEIQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKI		512 AVQALSKGVASNASDITRYTRPAAPLIQELRSIDQGLMLSWRSDVNSRQDRYE	940 VSAPRHSQKVDSQTIPKHVPEHTFHRLEAGEQYQIMIASVSGSLKNQINVVGRTV-PASV	QGVIADNAYSSYSLIVSWQKAAGVAERYDI ::: :::		1053 EDLTPGKKYKIQILTVSGGLFSKEAQTEGRTVPAAVTDLRITENSTRHLSFRWTASEGEL	1113 SWINIFLYNPDGNLQERAQVDPLVQSFSFQNLLQGRWYKM-VIVTHSGELS	736 DFYTLKWWPTDEEDRVBFKNVTQLEDLSSPSVRIPIEDLSPGRQYRFEVQASSNGIRS	1163 NESFIFGRTVPASVSHLRGSNRNTTDSLWFNWSPASGDFDFYELILYNP :	NGTKKENWKDKDLTEWRFQGLVPGRKYVLWVVTHS	850 TIKDKEKLANDTERKLSFSGLTPGKLYNVTVWTVSGGVASLPVQRLYRLHPLPISDLKAI		910 OVAARKEITLEMWIAFAGGEIIDFELGILSANDERAFGLLOONVIKNIETILOGGLKFIANIIF 1331 NVKTVSGDSWKTXSKPIFGSVRTKPDKIONLHCRPONSTALAGSW	TVVVRSGSIQGTDFADVSVSTLM			1431 GMTSEVVEDGTITMIDRPPPPPHIRNDEKDVLISKSSINFTVNCSWFSDTNGAVERFTV 1.	1491 VVREADGSDELKPEOOHPLPSYLEYRHNASIRVYOTNYFASKCAENPNSNSKSF
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Shenoy, Suresh
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Rastelli, Luca
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Best Local Similarity 29.3%; Pred. No. 1.1e-84;
Matches 455; Conservative 257; Mismatches 662; Indels 180;
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 220
SOFTWARE: CLYASEQLIST VERSION 0.1
SEQ ID NO 41
LENGTH: 1767
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US-10-087-684-41
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--YSKPIFGSVRT---KPDKIQNLHCRPQNSTAIACSW-IPP---DSDFDGY
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Publication No. US20040029222A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit
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Gerlach, Valerie
Grosse, William
Alsobrook II, John
Lepley, Denise
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Burgess, Catherine
Casman, Stacie
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Millet, Isabelle
Ellerman, Karen
Stone, David
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Search completed: March 10, 2006, 19:06:41 Job time : 203.859 secs
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APPLICANT: Zeringen, Bryan
APPLICANT: Zeringen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Malyankar, Uriel
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-214
CURRENT FILING DATE: 2000-08-14
CURRENT FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR PELING DATE: 2001-08-20
NUMBER OF SEQ. ID NOS: 216
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                   LENGTH: 1767
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TVSGGLFSKEAQTEGRTVPAAVTDLRITENSTRHLSFRWTASEGELSWYNIFLYNPDGNL 1126
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                              SDVFIANAGHEQGQDETIT----LSYTPTPADSTRFDIYRFSMGDPTIKDKEKLANDTER 863
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications make up the Published Applications make up the Published Applications and Applications applications make up the Published Applications and Applications and Applications and Applications and Applications and Applications and Applications are applications and Applications and Applications and Applications are applications and Applications and Applications and Applications and Applications and Applications and Applications and Applications and Applications and Applications and Applications are applications and Applications and

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions frapbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions

rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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Appl Appl Appl Appl Appl

Perfect score:

Sequence:

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Scoring table:

Minimum DB Maximum DB

Database

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Sequence 33, Application US/11112304A

Publication No. US20060002931A1

GENERAL INFORMATION:

APPLICANT: AMGEN, INC.

APPLICANT: AMGEN, INC.

APPLICANT: Ranchers, James

APPLICANT: Ranchers, James

APPLICANT: Ranchers, James

APPLICANT: Ranchers, James

APPLICANT: Ranchers, James

APPLICANT: Ranchers, James

APPLICANT: Ranchers, James

CURRENT REFERENCE: 3447

CURRENT PLING DATE: 2005-04-22

PRIOR APPLICATION NUMBER: US 60/565,158

PRIOR PLILING DATE: 2004-04-23

PRIOR PLILING DATE: 2004-04-13

PRIOR FILING DATE: 2004-05-14

PRIOR FILING DATE: 2004-05-14

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PRIOR FILING DATE: 2004-05-14

PRIOR PRIOR PRICE PRIOR UNDER: US 60/585,686

NUMBER OF SEQ ID NOS: 33

SEQUID NOS: 33

SECTION OF SEQ ID NOS: 33

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11.8%; Score 1242; DB 7; Length 1
Best Local Similarity 29.6%; Pred. No. 7.2e-75;
Matches 397; Conservative 190; Mismatches 503; Indels
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US-11-193-869-17

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US-11-090-561-627

US-11-193-781-19

US-11-193-781-19

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/cgn2_6/ptodata/2/pubpaa/USO6_NBW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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US-11-097-728-6

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Maximum Match 100%
Listing first 45 summaries
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Sequence 851, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FEASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1149 MYKMVIVTH--SGELSNESFIFGRTVPASVSHLRGSNRNTTDSLWFNWSPASGDFDF-YE 1205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1089 TDLRITENSTRHLSFRWTASEGELSWYNIFLYNPDGNLQERAQVDPLVQSFSFQNLLQGR 1148
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                                                          1305 SKVDLIYONTTAMTIYENLAP 1325
                        1970 RS----EQENPLFPIYENVNP 1986
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ORGANISM: Homo sapiens
US-10-995-561-851
                                                                                                                                          RESULT 2
US-10-995-561-851
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LENGTH: 1178
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ACSWIPPDSDFDGYSIECRKWDTQEVEFSRKLEKEKSLININMLVPHKRYLV	VLKWTCPPGANAGFELEVSSGAWNNATHLESCSSENGTEYRTEVTYLNF	SIKVQSAGMTSEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDT	RHNASIRVYOTNY		NSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQ-	LGYYNGKL	LPDEDLKEFTKPLYSDTFFSLPITTESEPLFGAIEGVSAGLFLIGMLVAVVALLIC	IIDGAESYVSFSRYSDA-VSLPQDPGVICGAVFGCIFGALVI-	RQKVSHGRERPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKIN		DSNYLLSKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPYDATRVKLSNVDDDPCSDY	DSNCGFAEEYEDLKLVGISQPKYAAELAENRGKNRYNNVLPYDISKVKLS-VQTHSTDDY	INASYIPGNNFRREYIVTQGPLPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWP	INANYMPGYHSKKDFIATQGPLPNTLKDFWRMVWEKNVYAIIMLTKCVEQGRTKCEEVWP	ADQDSLYYGDLILQMLSESVLPEWTIREFKICGEEQLDAHRLIRHFHYTVWPDHGVPETT	SKQ-AQDYGDITVAMISEIVLPEWIIRDFIVKNIQTSESHPL-RQFHFTSWPDHGVPDIT	QSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVH	DLLINFRYLVRDYMKQSPPESPILVHCSAGVGRTGTFIAIDRLIYQIENENTVDVYGIVY	DLRLHRVHMVQTECQYVYLHQCVRDVLRARKLRSEQENPLFPIYENVNP	DERMHRPLANOTEDQYVFLNQCVLDIVRSQKDSKVDLIYQNTTAMTIYENLAP		7.37	Sequence 3/, Application 05/11143584A Publication 05. US20060014180A1	InFORMATION: PANT: Bristol-Myers Squibb Company	TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHO FILE REFERENCE: D0072 DIVI	10MBER: 1		60/280,18	3-01 1-01	0S 5-05		NUMBER OF SEQ 1D NOS: 208 SOFTWARE: Patentin version 3.2	50.2	Mus musculus 1.37	•
1	Db 581	Oy 1424 Db 636	1	ΩD 688	Qy 1540	Db 740	Qy 1587	Db 791	Oy 1643	Db 841	Oy , 1698	Db 877	Qy 1758	Db 936	Qy 1818	966 qa	. Qy 1878	Db 1054	Qy 1938	Db 1114	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	US-11-143-984A-37		APPLIC	TITLE FILE F		PRIOR	PRIOR		PRIOR	PRIOR	; SOFTWARE:	LENGTH: 1705	; TYPE: PKT ; ORGANISM: Mus US-11-143-984A-37	

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1189 SLWFNWSPASGDFDFYELILYNPNGTKKENWKDKDLTEWRFQGLVPGRKYYLWVVTHSGD 1248
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DETITMIDEPPPPP LVCTYSAEVWHPPELAEA ADGSDELKPEQOHDLPSY TINMTLAPPGAINTY ESLGGKRDPTQQKFCDGPDCDNTQE-ICNGHDCDNTQE-ICNGH ITTESEPLFGALEGVSAG	1428 GSAG-WTSEVVEDSTITMIDREPPPPP 906 LGGNRQWSRAVTLVCTTSAEVWHPELAAER	QSAG-MTSEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTN 1482 QSAG-MTSEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTN 1482	GAVKYFTVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQTNYFASKCAENPNSN 1540 Qy 477 HANETSLEISIMWQTPVAEWEKYIISLADRDLLLIHKSLSKDAKEFTFTDLVP 527	SKEFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAXRISIRAFTQLFDEDLKEFT 1596	CANONIENSE CAN	CSIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKEYEELKEV 1713	GRNQSCDIALLPENRGKONRYNNILPYDATRVKLSNVDDDPCSDXINASYIPGNNFRREYI 1773 Qy 705 GRLYTVTITTRSGKYENHSFSQERTVPDKVQGVSNSARSDYLRVSW 752	VTGGPLPGTKDDFWRAVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQML 1833 Qy 753 VHATGDFDHYEVTIKNRNNFIQTKSIPKSENECVFVQLVPGRLYSVTVTTKSGQYEANEQ 812	SESSULPEWITREFXI-CGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYIN 1892 Qy 813 GNGRIIPEPVKDLTLRNRSTEDLHVTW-SGANGDVDQYEIQLLFNDMKVFPPFHL 866	A	YVYLHQCVRDVLRARKIRSEQENPLFEPIYENVN		Qy 1038 LRNTSE-PATTKQHKFEDLIPGKKYKIQILIVSGGLFSKEAQTEGRTVPAAVTDLRITEN 1096 	1143984A A1 A1	NG NOVEL HUMAN PHOSPHATASES OY 1157	셤 ~	DD 749ELLVSMQAGSAVVNLAMPSGP-LIGQGACHAQLS	Qy 1277 LAITWKGPPDWTDYNDFELQMLPRDALTVFNPYNNRKSEGRIVYGLRPCRSYQFN ::	5 781 DAGHLSWEQPLACQELFWIRDLTFGHTISMS 812 60/300,465 OV 1332 VKTVSGDSWKTYSKDIFGSVRTKPDKIQNLHCRPQNSTAIACSWIPPDSDFDGYS 1386	2 Db 813	Qy 1387 IEC-ŖKMDTQEVEFSRKLEKEKSLĻNIMMLVPHKRYLVŞIKYQSAGMT-ŞEVVEDSTIŢM 1444
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                                                                                                               TE-----DCDNTQE-ICNGRLKSGFQYRFSVVAFSRLNTPETILAFSAFSEPRASISLA 1074
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| SAMHPPELAEPPQVELG-----TGMGVTVVMRGMFGKDDGQ1QWYGIIATINMTLAQ 975
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOS
FILE REPRENCE: D0072 DIVI.
CURRENT APPLICATION NUMBER: US/11/143,984A
CURRENT PILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/256,868
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: US 60/295,848
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
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SOFTWARE: PatentIn version 3.2
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llarity 24.0%; Pro
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  Best Loca
Matches
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; TYPE: PRT ; ORGANISM: Homo sapiens US-11-000-463-250	7.9%; Score 832; DB 7; Length 1907;	vative 244; KYMATVTSISGDI	Db 10 TWVPLVPALVMLGLVAGAHGDSK-PVFIKVPEDQTGLSGGVASFVCQATG 58 Ov 581 DVEFYOVLLIHENVVIKNESISSETSRYSFHSLKS 615	: : : : : : : : :	Qy 616 GSLXSVV-VTTVSGGISSRQVVVGGRTVPSSVSGVTVNNSGRNDYLSVSWLVAPGDVDNY 674	675 EVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVIITTRSGK : : :- :: : : :	Db 177PATSNGRIKQLRSGALQIESSEESDQGKYECVATNSAGTRYSAPANLY-VRVRRVAPR 233 Qy 719 YENHSFSQERTVPDKVQGVSVSNSARSDYLRVSWVHATGDFDHYEVTIKNKNNFIQ 774	: ::	OY 775 TKSITEKSENECVFVQEVPGRIZSVTVTTKSGQYEANEGGNGRITEPEVKATED 834 1 : :	Qy 835 LHVTWSGANGD-VDQYEIQLENDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTI 891	892 SGDVQQSAFIEGFTVPSAVKNIHISPNGATDSLTVNMTPGGGDVDSYTVSAFRHS 193 NSIGRGPPSEAVRARTGEQAPSSPPRRVQARMLSASTMLVQWEPPEEPNGLVRGYRVY	Qy 947 QKVDSQTIPKHVFEHTFHRLEAGEQYQIMIASVSGSLKNQIN 988	QY 989 VVGRTVPASVQGVIADNAYSSYSLIVSWQKAAGVAERYDILLILTENGILL 1038	OY . 1039RNTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFSKEAGTEGRTVPAAV 1088 DD 553 EDQQHKVTFDPTSSYTLEDLKPDTLYRFQLAARSDMGVGVFTPTIEARTAQSTPSAPP 610	TDLRITENSTRHLSFRWTASEGELSWYNIFLYNPDGNLQERAQVDPLVQSFSFQN	1144 LLQGRMYKMVIVTHSGELSNESFIFGRTVPASVSHLRGSNRNTTDSLWFNW-	Db 671 LVGLEKWTEYRVWVRAHTDVGPGPESSPVLVRTDEDVPSGPPRKVEVEPLNSTAVHVYWK 730	LPVPSKQHGQIRGXQ-VTXVRLENGEPRGLPIIQDVMLAEAQWRPERSEDYETIS	1231 GLVPGRKXVLWVVTHSGDLSNKVTAESRTAPSPPSLMSFADIANTSLAITWKGP-	Db 786 GLTPETTYSVTVAAXTTKGDGARSKPKIVTTGAVPGRPTWMISTTAMNTAL-LQWHPPK 844 Qy 1285	Db 845 ELPGELLGYRLQYCRADEARPNTIDFGKDDQHFTVTGLHKGTTYIFRLAAKNRAGLGEEF 904	Qy 12911315
Db 749 ADFPEVFCQQVGSSQKTKLQEPVAVSSHVVTI780 Qy 1545 NIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISTRAFTQLFDEDLKEFTKPLYSDTF 1604	781	DD 807 IAVSTWVIEWNEWNVVISVLAILSTLIGHTLVYLIILRKKGH.QMARECGAGTFVNFA 864	Qy 1658 SIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKEYEELKDVGRNQ 1717 :	1718 SCDIALLPENRGKORYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQG	DD 925 PHFAADLPLANCKORYTNILPYDFSRVRLVSAMREEGADYINANYIPGYNSPQEYIATQG 984 Qy 1778 PLPGTKDDFWKAVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSFSV 1837	985 PLPETRNDFWKWVLQQKSQIIVMLTQCNEKRRVKCDHYWPFTEBPIAYGDITVEMISEEB	Qy 1838 LPEWTIREFKICGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSP 1895	GAGPTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVY	1956	Db 1160 IHQCVQLMMMKKKQQPCISDVIYENVS 1186	RESULT 6 US-11-000-463-250 ; Sequence 250, Application US/11000463 ; Publication No. US20050266423A1	<pre>// GENERAL INFORMATION: // APPLICANT: Tang, Y Tom // APPLICANT: Liu, Chenghua // APPLICANT: Asundi, Vinod</pre>	<pre>; APPLICANT: Chen, Rui-hong ; APPLICANT: Qian, Xiaohong B. ; APPLICANT: Weng, Zhiwei ; APPLICANT: Wehrman, Tom</pre>	; APPLICANT: Zhang, Jie ; APPLICANT: Zhou, Ping ; APPLICANT: Cao, Yi-Cheng ; APPLICANT: Drmanac, Radoje T.	 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REPERENCE: 78 FOSCIP4CN CURRENT APPLICATION NUMBER: US/11/000,463 CURRENT FILING DATE: 2004-11-29 	; PRIOR APPLICATION NUMBER: 10/291,265 ; PRIOR FILING DATE: 2002-11-08 ; PRIOR APPLICATION NUMBER: PCT/US01/02623	; PRIOR FILING DATE: 2001-01-25 ; PRIOR APPLICATION NUMBER: 109/922,279 . DBIOD BILING DATE: 2001-08-03	FRIOR FILING DATE: 2001-091, 404 PRIOR APPLICATION NUMBER: 09/491, 404 PRIOR FILING DATE: 2000-01-25	; PRIOR APPLICATION NUMBER: U9/61/, /46 ; PRIOR FILING DATE: 2000-07-17 ; PRIOR APPLICATION NUMBER: 09/631,451	; PRIOR FILLING LATE: 2000-094-03; ; PRIOR PLICATION NUMBER: 09/633,870; ; PRIOR FILLING DATE: 2000-09-15	; NUMBER OF SEQ ID NOS: 944 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEO ID NO 250	, LENGTH: 1907

US-10-821-234-1635

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1020 VAAAMKTSVILISWEVPDSYKSAVPFKILYNGQSVE---VDGHSM---RKL-----IA 1065
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                                                                                                                                                                                                                            CRPQNSTAIACSWIPPDSD-----FDGYSIECRKMDTQEVEFSRKLEKEKSLLNIM 1413
                                                                                                                                                                                                                                                                                                                                                                              MLVPHKRY--LVSIKVQSAGMTSEVVEDSTITMIDRPPPPPPPHIRVNEKDVLISKSSINF 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1472 TVNCSWFSDTNGAVKYFTVVVREADGSDELKPEQQHP----LPSYLE----YRH 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSLVRWF-----YIVVVPIDRVGGSMLTPRWSTPEELELDELLEAIEQGGEEQRRRR 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1518 NASIRVYQTNYFASKCAENPNSNSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAY 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RISIRAFTQLFDEDLKEFTKPLYSDTFF--SLPITTESEPLFGAIEGVSAGLFLIGMLVA 1635
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EKEIRTPEDLPSGFPONLHVTGLTTSTTELAWDPPVLAERNGRIISYTVVFRDINSOOEL 964
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Town
TITLE OF INVENTION: Methods for Diagnosis and Treatment of
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
FRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
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Publication No. US20050255114A1
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 1635
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TYPE: PRT ORGANISM: Homo sapiens

LENGTH: 1897

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-QGRMYKMVIVTHS--GELSNESFIFGRT---VPASVSHLRGSNRNTTDSLWFNW---- 1194
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                                    75;
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                                                                                                                                        619
                                                                                                                                                             SHDGKVVQ----SLVIAKSVR-----ECSFSS-----LTPGRLYTVTITTRSGKYENH 722
                                                                                                                                                                                                                                                                                                                  227
                                                                                                                                                                                                                                                                                                                                                                        894 DVQQSAFIE---GFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVD 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRRPPNAWHKHNTDAGLLTTVGSLLPGITYSLRVLAFTAVGDGPPSPTIQVKTQQGVPAQ 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          665 EKWTEYRVWYRAHTDVGPGPESSPVLVRTDEDVPSGPPRKVEVEPLNSTAVHVYWKLPVP 724
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                                                                                                                                                                                                                                                                                                                                                   SFSQERIVPDKVQGVSVSNSARSDYLRVSWVHATGDFDHYEVTIKNK----NNFIQTKSI
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                                                                                                   4 LVPALVMLGLVAGAHGDSK-PVFIK---VPEDQT-----GLSGGVASFVCQATGEPKP
                                                                                                                                        ------VEF----YQVLLIHENVVIKNESISSETSRYSFHSLKSGSLY
                                                                                                                                                                                                           SVV-VTTVSGGISSRQVVVEGRTVPSSVSGVTVNNSGRNDYLSVSWLVAPGDVDNYEVTL
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                                                                    525 LVPGRKYMATVTSISGDLKNSSSVKGRTVPAQVTDLHVANQGMTSSLFTNWTQAQGD-
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Query Match 7.9%; Score 826; DB 6; Length 1897; Best Local Similarity 23.5%; Pred. No. 1e-46; Matches 407; Conservative 244; Mismatches 670; Indels 410;
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-----VYGLRPGRSYQFNVKTVSGDSWKTY-SKPIFGSV--RTKPDK---IQNLHCRPQ 1366
                              1367 NSTAIACSWIPPDSD-----FDGYSIECRKMDTQEVEFSRKLEKEKSLLNIMMLVP 1417
                                                                                                                                                         1014 MKTSVLLSWEVPDSYKSAVPFKILYNGQSVE---VDGHSM---RKL------IADLQP 1059
                                                                                                                                                                                                                 1418 HKRY--LVSIKVQSAGMTSEVVEDSTITMIDRPPPPPPPHIRVNEKDVLISKSSINFTVNC 1475
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Publication No. US20060014180A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING NOVEL HUMAN PHOSPHATASES
FILE REFRENCE: DO072 DIV.
CURRENT APPLICATION NUMBER: US 60/26,868

PRIOR APPLICATION NUMBER: US 60/280,186

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2001-05-01

PRIOR FILING DATE: 2001-05-01

PRIOR FILING DATE: 2001-05-01

PRIOR FILING DATE: 2001-05-01

PRIOR FILING DATE: 2001-06-05

PRIOR PRIOR APPLICATION NUMBER: US 60/295,848

PRIOR PRIOR APPLICATION NUMBER: US 60/295,848

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

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PRIOR FILING DAT
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Sequence 47, Application US/10528031

Publication No. US20050262577A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GUelly, Christian
APPLICANT: Guelly, Christian
APPLICANT: Edelly, Christian
APPLICANT: Edelly, Christian
APPLICANT: Edelly, Christian
APPLICANT: Edelly, Christian
APPLICANT: Edelly, Christian
APPLICANT: Edelly, Christian
APPLICANT: Buck, Charles R.
TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for the TITLE OF INVENTION: prevention, diagnosis or treatment of liver disorders and epithell FILE REFERENCE: Oridis Biomed
CURRENT APPLICATION NUMBER: US/10/528,031

CURRENT FILING DATE: 2005-03-16

NUMBER OF SEQ ID NOS: 73

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOSCDIALLPENRGKURYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVT 1775
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LIGLL--LVTLVILRKKHLQMARECGAGTFVNFASLEREGKLPYSWRRSVFALLTLLPSC
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                                                                                                                                                                           Query Match 7.4%; Score 780.5; DB 7; Best Local Similarity 43.5%; Pred. No. 1e-44; Matches 171; Conservative 69; Mismatches 106;
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; LENGTH: 405
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-143-984A-28
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT PPLICATION NUMBER: US,10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1102

APPLICANT: Labat, Ivan APPLICANT: Stache-Crain, Birgit

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TENSTRHLSFRWTASE---GELSWYNIFLYNPD-----GNLQERAQVDPLVQSFSFQNLL 1145
                                                                                                            1146 QGRMYKWVIVTHS----GELSNESFIFGRT-VPASVSHLRGSNRNTTDSLWFNWSPASGD 1200
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                                                                   180 RMLSSTTILVQWKEPEBEPNGQIQGYRVY-YTMDPTQHVNNWMKHNVADSQITTIG--NLV 236
                                                                                                                              121 KEIDGIATTR-YSVAGLSPYSDYEFRVVAVANNIGRGPASEPVLTQTSEQAPSSAPRDVQA 179
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986 QINVVGRTVPAS----VQGVIADNA-------YSSYSLIVSWQKAAGVAERYDIL 1029
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                                                                                                                                                                                          OCSAIGRIVAGDRLWLOGIDVRDAPLKEIKVTSSRRFIASFNVVNTTKRDAG---KYRCM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VKLİLMNPEĞRKES------QEL-----IVQTDBDLPGAVPT 487
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                                                                                                                                                                                                                                                                               262 IRTEGGVGISNYAELVVKEPPVPIAPPQLASVGATYLWIQLNANSINGDGPIVAREVEYC
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                                                                                                          Indels 429;
                                                              Length 1452;
                                                                 Query Match 6.9%; Score 718.5; DB 6; Best Local Similarity 22.4%; Pred. No. 1.1e-39; Matches 269; Conservative 164; Mismatches 338;
                                                                                                                                                                                                                                   1030 LLTENGILLRNTSE------
ORGANISM: Homo sapiens
                          US-10-821-234-1102
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Sequence 1102, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:

RESULT 10 US-10-821-234-1102

Db 557 YPGTTYSFIKASTAKGFGPPVTTRIATKISAPSMPEYDTDTPLNETDTTITVML 611 Qy 1476 SWFSDTNGAVKYFTVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQTNY 1528 C12 KPAQSRGAPVSVYQLVVKEERLQKSRRAADIIECFSVPVSYRNASSLD-SLHY 663 Qy 1529 FASKCAENPNSNSKSFNKLGAEMSSLGCKRDFTQQKFCDGPLKPHTAYRISIRAFTQLF 1588	1627 LFLIGMLVAVVALLICRQKVSH	11	Qy 1863 FHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRILQ 1922 Db 1067 FHFTSWPDHGVPCYATGLIGFVRQVK-FLN-PPEAGPIVVHCSAGAGRTGCFIAIDTMLD 1124 Qy 1923 QLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVYLHQCV 1960 SISSULT 1125 MAENEGVVDIFNCVRELRAQRVNLVQTEEQYVFVHDAI 1162		; NUMBER OF SEQ ID NOS: 14 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2 ; LENGTH: 2314 ; TYPE: PRT ; ORGANISM: Homo Sapiens US-11-097-728-2	Query Match 6.6%; Score 687.5; DB 7; Length 2314; Best Local Similarity 21.2%; Pred. No. 2.7e-37; Matches 466; Conservative 321; Mismatches 763; Indels 653; Gaps 106; Qy 176 GSKYNIAITAVSGGKRSFSVYTNGSTVPSPVKDIGISTKANSLLISWSHGSGNVERYRLM 235
QY 1651 ERPSARLSIRRDRPLSVH	1755 SDYINASYIPGNNFRREXIVOGPLPGTKDDFWRWWWEQNYHNIVMYTQCVEKGRVKCDH 11	QY 1933 YGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLRARKLRSEQENPLFPIYENVN 1985 Db 1124 YNCVRELRSRRVNMVQTEEQYVFIHDAILEACLCGDTSVPASQVRSLYYDMN 1175 RESULT 11 US-11-080-991-22 ; Sequence 22, Application US/11080991 ; Publication No. US20050266437A1	; GENERAL INFORMATION: ; APPLICANT: Veiby, Petter Ole ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR ; TITLE OF INVENTION: COMPOSITION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST ; TITLE OF INVENTION: AND OVARIAN CANCER ; FILE REFERENCE: MRI-039 ; CURRENT APPLICATION NUMBER: US/11/080,991 ; CURRENT PILING DATE: 2005-03-11 ; PRIOR FILING DATE: 2002-06-21 ; NUMBER OF SEQ ID NOS: 112	SOFTWARE: FastSEQ for Windows Version 4.0 SEQ 1D NO 22 LENGTH: 1463 TYPE: PRT ORGANISM: Homo sapiens G.64; Score 691.5; DB 7; Length 1463; Guery Match	Qy 1268 SFADIANTSLAITWKGPPDWTDYNDFELGWLPRDALTVFNPYNNRKSEGRIVY 1320 Db 394 EIVDIRARQLTLGWE-PFGYAVTRCHSYNLTVQYQYVFNIQQQYEAEEVI 441 Qy 1321GLRPGRSYQFNVKTVSKDSWKTYSKPIFGSVRTKDDKIQNLHCRPQ 1366 Db 442 QTSSHYTLRGLRPFWTIRLRL-LLSNPEGRRESEELVVQTEEDVPGAVPLESIQGGPF 498	Qy 1367 NSTAIACSWIPPDSDFDGYSIECRKMDTQEVEFSRKLEKEKSLLNIMML 1415 b 499 EE-KIYIQWKPP-NETNGVITLYEINYKAVGSLDPSADLSSQRGKVFKLRNETHHLFVGL 556 , Qy 1416 VPHKRYLVSIKVQSAGMTSEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNC 1475

938 HIFTVSYSSAI 1108 SEGELSWYN : : 992 GDGEWSGASSE 1164 ESFIFGR 1044 SEIIYGNETEI		1346 PIFG-SVRTKE 1256 SLQGLTISYAS 1403 LEKEKSLLNIW : : 1316 VLSIDEPLNTI 1457 VNEKDVI : : :	1506 QHPLPSY 1434 DGLSIHKCMSC 1550 AEMESLGGK 1593 SQTCMDRSPCK 1592 1547 ESGSGQGTSDS	1607 VFHVSEAEASN 1646VSHGRERPS 1665 FQTAHFYLEDS 1704 SKEYELKDVG 1717 TEEFETLKEFY 1753 PCSDYINASYI 1753 RCSDYINASYI 1777 KLTDYINANYV	1813 DHYWPADQDSI 1837 DQYWPAD-GSE 1866 TVWPDHGVPET 1896 TQWPDMGVPEY 1926 SKDSVDIXGAV 1954 HEGTVNIFGEI
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ESTIGNB-TELLYNPACTIKEENMY-DEDICTEMEPOGLYDERKYVI-MAVTHSGDLSINKPOSLAHTTIKUPDHEISG		10	SELSWYNIFLYNPDGNLQERAQVDPLVQSFSFQNLLQGRMYKWVIVTHSGELSN 116
BESTEGRTVPASVSILRGSNRNTTDSLWFNWGDRAGD SEITIGNETELQIPSPNEMYYPSESTYWPNMYDNWLANSLÓGTSVSISGTKGMF DFYELILIYNPHOTKKENWK-DKOLTERRPOGLYPGRKYVLWYTHSGDLSNK		6	ALSK 104
SELINGHEROLDÉSPHENVYPSESTYMPNMYDNÍNKLAALÚGETSVÍTŠSTKÁH- DPYELILIYMPNGTKKENMK-DROLTENRFOGLUPGRKYVLMYVTHSGDLSNK		16	SFIEGRTVPASVSHLRGSNRNTTDSLWFNWSPASGDF 12
DPTELLILIYNPUGTKKENWKDKOLTEWRFOGLUPGEKKYULWVTHSGBLSNK		9	
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LÄÄNÄEPÄSÖPÄSSEMLSPSTQLEYETSÄSFÄFEVLLQPSFQASÖVOTLLKTVÜPANÜ RDALTVDNPNUNRKSBERIVYGLRPGRSYOFWKTVSGDSWKTYSK SPPILATERVOKISSTMLHLIVSNBASSENNLHSTSVPPUSDTS-HPHAS PITG-SWRTKPDRIONLHRPONSTALISML		25	129
RDALTVENPTWARKSEGRIVYGLRPGRSYGFWYKTVSGDSWKTYSK SPITIAL SONGERSTALLILVSSASGRIVTSCAREGERINGTOFTER SPITIAL SONGERSTALLILVSSASGRIVTSCAREGERINGTOFTER SPITIAL SONGERSTALLILVSSASGRIVTSCAREGERINGTOFTER SPITIAL SONGERSTALLILVSSASGRIVTSCAREGERINGTOFTER SPITIAL SONGERSTALLILVSSASGRIVTSCAREGERINGTOFTER SPITIAL SONGERSTANDAYSTRYOSAGRIT-STANDERPPEPHIR WESTELLANDAM-LUPHKRYLYSKOSAGRIT-SEGSTORTOFTERSTEP STANDELLANDAM-LUPHKRYLYSKOSAGRIT-SEGSTORTOFTERSTEP STANDELLANDAM-LUPHKRYLYSKOSTORTOKTYVVREADGSDELKFPG STANDELLANDAM-LUPHKRYLYSKOSTORTOKTYVVREADGSDELKFPG STANDERSTALLINGTHERSTKAT-SEGSTORTOKTYVTTOKTYVYREADGSDELKFPG STANDERSTALLINGTHERSTKAT-SEGSTORTOKTYVTTOKTYVY		14	120
SPPIIVETPKYDKISSTMIHLIVSNGASSĖRNMIHŠTSVPŲPDVŠPPIŠ-HPHÄŠA PIFG-SVRIKEDDKIQNIHGERDNSTALACSWIPPDSDEDGYSIEGRKWDTOGVE-FSRK SIGHTIS SASEKTSPPILKESSSHQVVPSLYSNDELFGTANLEINQAPPPKGRHVPATP LEKEKSLIANDAM-LUPHKRYLVSIKVOSAGMTSEVVEDSTITMIDRPPPPPHIR VASIDEPLINTLINKLIHSDEILTSTKSSTGKVFAGIPTVASDTTSVSTDHSVPIGKGHVA VNEKDVLISKSSINFTVNCSWFSDTNGAVKTPTVVVREADGSDELKPEG SIGHTIS SASEKTSPENTALINKLIHSDEILTSTKSSTGKTFAGIPTVASDTTSVSTDHSVPIGKGHVA VNEKDVLISKSSINFTVNCSWFSDTNGAVKTPTVVVREADGSDELKPEG SIGHT STANSPHAGGSTSTKLLFPSKATSELSHAÄNSDAGHVGGEDGDTDDGDDDDDRDG QHPLPSTLEKR		30	VYGLRPGRSYQFNVKTVSGDSWKTYSK 134
PIEG-SVRTKEDEKIONLHCREQNSTAIACSWIPPDSDEDGYSIECRKWDTGEVEFSRK		20	HSTSVPVFDVSPTS-HMHSA 125
SLOGATISTSYASEKYEPVLLKSESSHOVVPSLYSNJELPOTANIEINOAHPPKGRHVPATP ILEKEKSLLINIMA-LIVPHKRYLVSIKVQSAGMTSEVVEDSTITMIDBPPPPPHIR ILEKEKSLLINIMA-LIVPHKRYLVSIKVQSAGMTSEVVEDSTITMIDBPPPPPHIR ILEKEKSLLINIMA-LIVPHKRYLVSIKVQSAGMTSEVVEDSTITMIDBPPPPPHIR ILEKEKSLLINIMA-LIVPHKRYLVSIKVQSAGMTSEVVEDSTITMIDBPPPPPHIR ILEKEKSLLINIMA-LIVPHKRYLVSIKSSYAGKVFRAGIPTVASDTFVSTDHSVPIGNGHWA ILEKASPHRDGSVTSTKLLFPSKATSELSHSAKSDAGLVGGEDGDTDDGDDDDBRDS ILEKASPHRDGSVTSTKLLFPSKATSELSHSAKSDAGLVGGEDGDTDDGDDDDBRDS ILEKASPHRDGSVTSTKLLFPSKATSELSHSAKSDAGLVGGEDGDTDDGDDDDBRDS ILEKASPHRDGSVTSTKLLFPSKATSELSHSAKSDAGLVGGEDGDTDDGDDDDBRDS ILEKASPHRDGSVTSTKLLFPSKATSELSHSAKSDAGLVGGEDGDTDDGDDDDBRDS ILEKASSCKASSEGKVMNDSDTHENSL		34	SVRTKPDKIQNLHCRPQNSTAIACSWIPPDSDFDGYSIECRKMDTQEVEFSRK
LEKEKSLIAINMA-LUVPHKRYLVSIKVOSAGWTSEVVEDSTITMIDRPPPPPPHIR 1 'L:	_	25	131
'VISIDEPLATLINGLINGLINGERIA'S STATES YOU'GVERGIPT'ASTITE'S TOUGH'A 1 'VISIDEPLATLINGLINGLINGERIA'S STATES YOU'GVERGIPT'ASTITE'S TOUGH'A 'NNEKDVLISKSINFTUNCSWFSDTNGAKYFTUVYFEADGSDELKPEQ ': : : : :		40	145
VNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVREADGSDELKFEQ 1 ITAVSPHRDGSVTSTKLIFPSKATSELSHSAKSDAGJVGGEDGDTDDDDDEDBED S QHPLEBSYLEYR QHPLEBSYLEYR QHPLEBSYLEYR Q		31	137
THAVSPHEGGSTTSTILLE PSKAT - SELSHS KSDAGUNGGEDGDTDDGDDDDBDBBBBBBCSTSTKLLE PSKAT - SELSHS KSDAGUNGGEDGDTDDGDDDDDBDBBBCOHPLASTRYCHYQTHY PASKCAENPINKLG		45	EKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVREADGSDELKPEQ 1
QHPLPSYLEYRHNASIRVYQTNYFASKCAENPNSNSKSFNIKLG DGLSIHKCMSCSSYRESQEKVMNDSDTHENSL-MDQNNPISYSLSENSEEDNRYTSVSSD AEMESLGGKRDPTQQKFCDG		37	: :: : : : : : : : : : : : : :
DELSIHKCMŠCSSYRESQEKVANDSDTHENŠI. MDQNNPISYSLSENSEEDNRYTSVSSD AE-MESLGGKRDPTQKFCDG		50	HPLPSYLEYRHNASIRVYQTNYFASKCAENPNSNSKSFNIKLG 154
AEMESLGGKRDPTQQKPCDGPLKPHTAYRISIRAFTQLFDED SITE SQTGMDRSPGKSPSANGLSQKHNDGKEENDIGTGSALLPLSFBS		43	SIHKCMSCSSYRESQEKVMNDSDTHENSL-MDQNNPISYSLSENSEEDNRVTSVSSD 149
SQTGMDRS PGKS PSANGLSQKHNDGKEENDIOTGSALLELSPESKAWAVLTSDE SQTGMDRS PGKS PSANGLSQKHNDGKEENDIOTGSALLELSPES		55	MESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDED 159
ESGSGGTSDSLANENETSTDESPADTHEKDADGILAAGDSEITPGFPGSPTSSTTSENSE LFGAIEG		49	GIGMDRSPGKSPSANGLSQKGNDGKEENDIQTGSALLPLSPGSKAWAVLTSDE 154
ESGSGQCTSDS.IAENETSTDFSFADTNEKDADGILAAGDSEITPGFPQSFTSSVTSENSE LF		59	FFSLPITTESEP 161
		54	SSGQGTSDSLNENETSTDFSFADTNEKDADGILAAGDSEITPGFPQSPTSSVTSENSE
VEHVSEARASNESHESRIGLAEGLESEKKAVIPLVIVÄÄLTÄTCLVVIVÄGLIIVWRKC 166 VSHGRERPSARLSTRADRESHLANGGKGNRKTSCPIKINGFGHFWALADLASSGF171 SKEYTAHFYLEDSTSPRVISTPPTFIFPISDDVGAIPIKHFPKHVADLHASSGF171 SKEYTELKDVGRN-OSCDIALLPENRGKNRYNNILPYDATRVKLANGLASSGF171 SKEYEELKDVGRN-OSCDIALLPENRGKNRYNNILPYDATRVKLANGLASSGF171 SKEYTELKDFRYGEVGSCTVDLGITADSSNHPDNKHKNRYINIVAYDHSRVKLANGLAEKDG 177 PCSDYINASYIPGNNFRREYIVTQGPLFGTKDDFWKMYWEQNYHNIVMYTQCVEKGRVKC 181		1616	164
VSHGEREPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFWKLQADSNYLL 170		1607	7
PGTAHPYLEDŠTSPRVISTPPTPIPDISDDVGAİPİKHFPKHVADLHÁSSGF 171 SKEYELKDVGRN-QSCDIALLPENRGKARYNNILPYDATRVKLANUDDD 175 :: : : : :		64	HINIGOKGNRKTSCPIKINOFEGHFMKLOADSNYLL 170
SKEYEELKDVGRN-QSCDIALLPENRGKNRYNNILPYDATRVKLSNVDDD 175 :: : : : : :		99	FPISDDVGAİPİKHFPKHVADLHASSGF 171
TEFFTLKEFYQEVQŚCTVDLGITADSSNHPDNKHKORYINIVAYDHSRYKLAQLAEKDG 177 PCSDYINASYIPGNNFRREYIVTQGPLPGTKDDFWKWWWEQNYHNIVWYQCVEKGRYKC 181		1704	SKEYEELKDVGRN-QSCDIALLPENRGKNRYNNILPYDATRVKLSNVDDD 175
PCSDYINASYIPGNNFRRYIVTGGPLPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKC 181		1717	TEEFETLKEFYQEVQSCTVDLGITADSSNHPDNKHKNRYINIVAYDHSRVKLAQLAEKDG 177
7 KLTDÝINÁNÝVDGYNRPKAÝÍAAĞGPÍKSÍAEDÍWRMÍWEHNVEVÍVMÍTNLVEKÖRRKČ 183 8 DHYWPADQDSLYYGDLILQMLSESVLPEWTIREFKICGEEQLDAHRLIRHFHY 186		75	181
13 DHYWPADQDSLYYGDLILQMLSESVLPEWTIREFKICGEEQLDAHRLIRHFHY 186 17 DQYMPAD-GSEEYGNFLYTQKSVQVLAYYTVNFTLRNTKIKKGGEGGEPGKTPGTFT 189- 180 DQYWPAD-GSEEYGNFLYTQKSVQVLAYYTVNFTLRNTKIKKGGGFGFGFGFTVTQYHY 189- 180 TWWPDHGVPETTGSLIQFVRTVRDYINRSPEAGFTVVHCSAGVGRTGFFTALDRILQQLD 192- 181		1777	183
54 HEGTVNIFGELKHIRSQRAYCHINESPEAGFORTURER ACCORDANGE AC		81	186
66 TVWPDHGVPETTQSIIQEVKTVRDYINKSPGAGPTVVVCGAGGGGFVFTALLALDUD 192 96 TQWPDMGVPEYSLPVLTFVRKAA-YAKRH-AVGPVVVHCSAGVGRTGTYIVLDSMLQQIQ 195 26 SKDSVDIYGAVHDLRLHRVHWQTECQYYVLHQCVRDVLRARK 1968 23 SKDSVDIYGAVHDLRLHRVHWQTECQYYVLHQCVRDVLRARK 1968 24 HEGTVNIFGFLKHIRSQRNYLVQTEEQYVFIHDTLVEAILSKE 1996	_	3	
26		86	192
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1457 VN----EKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVV-----READGSDELKPEQ 1505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1434 DGLSIHKCMSCSSYRESQEKVMNDSDTHENSL-MDQNNPISYSLSENSEEDNRVTSVSSD 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       956 KHVFEHTFHRLEAGEQYQIMIASVSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVS 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .016 WQKAAGVAERYDILLLTENGILLR-----NTSEPATTKQHKFEDLTPGKKYKI------ 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .064 QILTVS---------GGLFSKEAQTEGRTVPAAVTDLRITENSTRHLSFRWTA 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1108 SEGELSWYN----IFLYNPDGNLQERAQVDPLVQSFSFQNLLQGRMYKWVIVTHSGELSN 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1164 ESPIFGR----TVPA------SOSHLRGSNRNTTDSLWFNWSPASGDF 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1253 VTAESRTAPSPPS-----LMSFADIANTSLAITWKGPPDWTDYNDF---ELQWLP 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1300 RDALTVFNP------YNNRKSEGRIVYGLRPGRSYQFNVKTVSGDSWKTYSK 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1204 SDPILVETPKVDKISSTMLHLIVSNSASSENML-----HSTSVPVFDVSPTS-HMHSA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1346 PIFG-SVRTKPDKIQNLHCRPQNSTAIACSWIPPDSDFDGYSIECRKMDTQEVE--FSRK 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1403 LEKEKSLINIMM--LVPHKRYLVSIKVQSAGMT----SEVVEDSTITMIDRPPPPPPHIR 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             844 Q------VISATESDKVPLHA---SLPVAGGDLLLEPSLAQYSDVLS 881
                                                                                                                                                                                                                                                         GRTIPEPVKDLTLRNRSTEDLHVTWSGANGDVDQYEIQLLFNDMKVFPPFHLVNTATEYR 874
                          GTAE--SLNTVSITEYEEESLLTSFKLDTGAEDSSGSSPATSAIPFISENISQGYIFSSE
                                                                                                    613 NPETITYDVLIPESARNASEDSTSSGSEESLKDPSMEGNV------WFPSSTDI
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785 PAASSSDSALHATPVFPSVDVSFESILSSYDGAPLLPFSSASFSSELFRHLHTV-SQILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            938 HIFTVSYSSAIPVHDSVGVTYQGSLFSGPSH-----IPIPKSSL-ITPTASLLQPTHALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPGRL-YTVTI--TTRSGKYENHSFSQERTVPDKVQGVSVSNSARSDYLRVSWVHATGDF
                                                                                                                                                     DHYEVTIKNKNNFIQTK--SIPKSENECVFVQLVPGRLYSVTVTTKSGQYEAN----EQGN
                                                                                                                                                                                                                                                                                                            FTSLTPGRQYKILVLTI------SGD--VQQSAFIEGF--TVPSAVKN--IHIS
                                                                                                                                                                                                                                                                                                                                                                                         PNGATDSLTVNWTPGGGDVD-------SYTVSAFRHSQKVDSQTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     882 TTHAASETLEFG----SESGVLYKTLMFSQVEPPSSDAMMHARSSGPEPSYALSDNEGSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFYELILYNPNGTKKENWK--DKDLTEWRFQGLVPGRKYVLWVVTH-----SGDLSNK--
564 WLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMDKGIL----VH--GGVVDKHATS-YAFHGLSPGYLYNLTVMTEAAGLQNYRWKLVRTA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMEVSNLKVTNDGSLTSLKVKWQRPP-----GNVDSYNITLSHKGTIKESRVLAP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGRMRSLVVSWSPPAGDWEQYRILLFNDSVVLLNITVGKEETQ------YVMDDTGLVP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGSLT-----SPECTDTVDW--IVFKD-----TVSISESQLAVFCEVLTMQQSGYVM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 LMDY------LQNNFREQQYKFSRQVFSSYTGKEEIHEAVCSSEPENVQADPENYT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : | : | : | | : | | | : | | SLLVTWERPRVVYDTMIEKFAVLYQQLDGEDQTKHEFLTDGYQDLGAILNNLLLPNMSYVL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVTSISGDLKNSSSVKGRTVPAQVTDLHVANQGM-----TSSLFTNWTQAQGDVEFY 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVLLIH-----ENVVIKNESISSETSRYSFHSLKSGSLYSVVVTTVS------GG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Erik Feehr
APPLICANT: Sabine Muller
APPLICANT: Sabine Muller
APPLICANT: Sabine Muller
APPLICANT: Sabine Muller
APPLICANT: Daniel J. Chin.
ITILE OF INVENTION: MONOCLONAL ANTIBODIES DIRECTED TO RECEPTOR PROTEIN
ITILE OF INVENTION: TYROSINE PHOSPHATASE ZETA
ITILE OF INVENTION: TYROSINE PHOSPHATASE ZETA
ITILE OF INVENTION: TYROSINE PHOSPHATASE ZETA
ITILE OF INVENTION: TYROSINE PHOSPHATASE ZETA
ITILE OF INVENTION NUMBER: US/11/097,728
CURRENT APPLICATION NUMBER: 10/652,981
PRIOR PELING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTESQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GKCNMSSDGSEHSL--EGQKFPLEMQIYCFDADRFSSFEEAVKGKGKLRALSILFE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 VGTEENLDFKAIIDG-----VESVSRFGKQAALD-----PFILLNLLPNSTDKYYIY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QLRVKHANET 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLSIMWQTPVAEWEKYIISLA-----DRDLLLIHKSLSKDAKEF--TFTDLVPGRKYMA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWDKTSLENTFIHNTGKTVEINLTNDYRVSG-----GVSEMVFKASKITFHW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WITETH--FKELVPGRLYQVTVSCVS--GELSAQKMAVGRTFPDKVANLEANN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.6%; Score 687.5; DB 7; Length 2353;
llarity 21.2%; Pred. No. 2.8e-37;
Conservative 321; Mismatches 763; Indels 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 GRQYEVEVIVESGNLKNSERCQGRTVPLAVL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(2353)
...OTHER THORMATION: PTP-zeta SM2 23a exon variant US-11-097-728-6
                                                     Sequence 6, Application US/11097728
Publication No. US20050260132A1
GENERAL INFORMATION:
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466; Conserva
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14 LSLLOTGLAEPERCNFTLAESKASSHSVSIQWRILGSPCNF 54 	55 SLIYSSDTLGAALCPTERID	97 SLDEERTVVLQTDPLPPARFGVSKEKTTSTGLHVWWTPSSGKVTSYEVQLFDENNQKI 154	155 QGVQIQESTSWNEYTFFNLTAGSKXNIAITAVSGGKRSFSVYTNGSTVPS 204 : ::	205 PVKDIGISTKANSLLISWSHGSGNVERYRLMLMDKGIL-VHGGVVDKHATSYA 256	257 -FHGLSPGYLYNLTVMTEAAGLQNYRWKLVRTAPMEV-SNLKVTNDGSLTSLKVKWQRPP 314	315 GNVDSYNITLSHKGTIKESRVLAPWITETHFKELVPGRLYQVTVSCVSGELSAQK 369 	370MAVGRIFPDKVANLEANNNGRMRSLVVSWSPPAGDWEQYRILLFN 414 : : : : : : : :	415 DSVVLLNITVGKEETQYVMDDTGLVPGRQYEVEV-IVESGNLKNSERCQGRTVPLA-VLQ 472 ::: :: ::	473 IRVKHANETS-LSIMMQTPVAEWEKYIISLADRDLLLIHKSLSKDA 517	518 KEFTFTDLVPGRKYMATVTSISGDLKNSSSVKGRTVPAQVTDLHVANQCMTSSLFTNW 575 1230 SSCTFDNLSPGLEYNVSVYTVKDD-KESVPISFTIPEVPQLTDLSFVDI-TDSSIGLRW 1287	576 TQAQGD-VEFYQVLLIHENVVIKNESISSETSRYSFHSLKSGSLXSV-VVTTVSGGIS 631 1288 TPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYYTVTGLEPGIDYDISVITLINGGES 1347	632 SRQVVVEGRTVPSSSVSGVTVNNSGRNDYLSVSWLVAPG-DVDNYEVTLSHDGKVVQSL 688 : : :	689 VIAKSVRECSFSSLTPGRLYTVTITTRSGKYENHSFSQERTVPDKVQGVSVSNSAR 744 1406 SISPSDNAVVLTNLLPGTEXVVSVSSVYEQHESTPLRGRQKTGLDSPTGIDFSDITA 1462	745 SDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIPKSENECVFVQLVPGRLYSVTVT 801	TKSGQYRANEQ-GNGRTIPEPVKDLTLRNRSTEDLHVTWSGANG L : : : :	845 DVDQYEIQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEGF 904 :: : :: 1581 PVQEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPI 1625	905 TVPSAVKNIHISPNGATDSLITVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPK 956
& <u>4</u>	& 8	ර් සි	& g	ò a	& 8	è 8	6 G	& 6	ò 8	& 8	강 음	<i>&</i> €	ò 8	કે ક	8 & A	& a	\$ 90 \$
QY 1550 AEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDED 1591 :: :	Oy 1592	Oy 1616 LF	Qy 1646VSHGRERPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFWKLQADSNYLL 1703 1665 FQTAHFYLEDSTSPRVISTPPTFIFPISDDVGAIPIKHFPKHVADLHASSGF 1716	Qy 1704 SKEYEELKDVGRN-GSCDIALLPENRGKRRYNNILPYDATRVKLSNVDDD 1752 	Qy 1753 PCSDYINASYIPGNNFRREYIVTQGPLPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKC 1812	QY 1813 DHYWPADQDSLYYGDLJLQMLSESVLPEWTIREFKICGEGQLDAHRLIRHFHY 1865	Qy 1866 TWWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRILLQQLD 1925	Qy 1926 SKDSVDIYGAVHDLRLHRVHMVQTECQYVYLHQCVRDVLRARK 1968 : : :		; Sequence 15, Application US/11193561 ; Publication No. US20060024757A1 ; GENERAL INFORMATION: ; APPLICANT: Hussa, Robert	<pre>// APPLICANT: STOTTET, SIMON // TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti // FILE REFERENCE: 17101-080001/831 // CURRENT APPLICATION NUMBER: US/11/193,561</pre>	CURRENT FILING DATE: 2005-07-29 PRIOR APPLICATION NUMBER: 60/592,823 PRIOR FILING DATE: 2004-07-30 PRIOR APPLICATION NUMBER: 60/592,803		; PRIOR FILING DATE: 2004-07-30 ; PRIOR FILING DATE: 2004-07-30 ; PRIOR FILING DATE: 2004-07-30	NOWARE: FastSEQ for Windows Version 4.0 ; SOPTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 15 ; LENGTH: 2477 ; Type: PRT) ORGANISM: Homo Sapiens) PUBLICATION INFORMATION:) DATABASE ACCESSION NUMBER: GenBank NM 212482) DATABASE ENTRY DATE: 2005-06-10	OS-II-193-501-15 Query Match Best Local Similarity 20.0%; Pred. No. 1.9e-36; Matches 399; Conservative 321; Mismatches 769; Indels 505; Gaps 91;

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1135 SGSIVV-----SGLTPGVEYVYTIQVLRDGQERDAPIVNKVVTPLSPPTN 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 P-----VKDIGISTKANSLLISWSHGSGNVERYRLMLMDKGIL-VHGGVVDKHATSYA 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          739 ŚWVSAŚDTVSG-----PRVEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRKYIVNVYQI
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DATABASE ACCESSION NUMBER: GenBank NM 212482
DATABASE ENTRY DATE: 2005-06-10
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                CURRENT APPLICATION NUMBER: US/11/193,771
CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: 06/592,823
PRIOR FILING DATE: 2004-07-30
PRIOR PELING DATE: 2004-07-30
PRIOR PELING DATE: 2004-07-30
PRIOR PELING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 60/592,804
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PRIOR FILING DATE: 2004-07-30
    FILE REFERENCE: 17101-027001/828
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo Sapiens
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Publication No. US20060024722A1
GENERAL INFORMATION:
APPLICANT: Fisher-Colbrie, Mark
APPLICANT: Hickok, Durlin
APPLICANT: LaPointe, Jerome P.
TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
: | : | : | : | : | 1.29
1671 NGPGPIKTKTRAGPDQTEMTIEGLQPTVEYVSVYAQN-PSGESQPLVQTAVTNIDRPKGL 1729
                                                                                   1062 KIQILTVSGGLFSKE-AQTEGRTVPAAVTDLRITENSTRHLSFRWTASEGELSWYNIFLY 1120
                                                                                                                                                                                                                         1121 NPD--GNLOERAQVDPLVQSFSFQNLLQGRMYKMVIVTHSGELSNESFIFGRTVPASVSH 1178
                                                                                                                                                                                                                                                                                                                                 LRGSNRN--TIDSLWFNWSPASGDFDFYELILYNPNG-TKKENWKDKDLTEWRFQGLVPG 1235
                                                                                                                                                                                                                                                                                                                                                                                     1236 RKYVLWVVT-HSGDLSNKVTAESRTAPSPPSLMSFADIANTSLAITWK------ 1282
                                                                                                                                                                                                                                                                                                                                                                                                                 ----GPPDWTDYNDFELQWLPRDALIVFNPYNNRKSEGRIVYGLRPGRSYQFNVKTVSG 1337
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                                                          -----SLIVSWQKAAGVAERYDILLIT-ENGILLRNTSEPATTKQHKFEDLTPGKKY
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2391 KTYHVGEQWQKEYL 2404
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	SRQVVVEGRTVPSSVSGVTVNNSGRNDYLSVSWLVAPG-DVDNYEVTLSHDGKVVQSL 688 : : :		SISPSDNAVVLTNILIPGTEYVVSVSSVYEQHESTPIRGRQXTGLDSPTGIDFSDITA 1462	SDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIPKSENECVFVQLVPGRLYSVTVT 801 :: : :	TKSGQYEANEQ-GNGRTIPEPVKDLTLRNRSTEDLHVTWSGANG 844	alngreespiligogstvsdvprdlevvaatptsilismdapavtvryritygetggns 1580	DVDQYEIQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEGF 904	GSASIAIISGENFGVDIIIIVIAVIGKGDSFASSAFI	TVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPK 956 ::	HVFEHTFHRLEAGEQYQIMJASVSGSLKNQINVVGRTVPASVQGVIADNAYSSY 1010	: NGPGPTKTKTAGPDQTEMTIEGLQPTVEYVVSVYAQN-PSGESQPLVQTAVTNIDRPKGL 1729	SLIVSWQKAAGVAERYDILLIT-ENGILLRNTSEPATTKQHKFEDLTPGKKY 1061	AFTDVDVDSIKIAWESPQCQVSRXRVTYSSPEDGIHELPPAPDGEEDTAELQCIRPGSEY 1789	KIQILTVSGGLFSKE-AQTEGRTVPAAVTDLRITENSTRHLSFRWTASEGELSWYNIFLY 1120 		NPDGNLOERAQVDPLVQSFSFQNLLQGRMYKMVIVTHSGELSNESFIFGRTVPASVSH 1178 :			RKYVLWVT-HSGDLSNKVTAESRTAPSPPSLMSFADIANTSLAITWK 1282	::: : : : ::	GPPDWIDYNDFELQWLPRDALIVFNPYNNRKSEGRIVYGLRPGRSYQFNVKTVSG 1337	YEKPGSPPREVVPRPRPGVTEATIT-GLEPGTEVTIYVIALKN 2069	DSWKTYSKPIFGSVRIKPDKIQNLHCRPQNSTAIACSWIPPDSDFDGYSIECRKWDTQEV 1397	NOKSEPLIGRKKTDELPQLVTLPHPNLHGPEILDVPSTVQKT 2111	FFSRKLEKEKSILNIMMLVPHKRYLVSIKVQSAGMISEVVEDS 1440		TITMI-DRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVV 1492	TATPIRHRPRPYPPNVGBEIQIGHIPREDV	READGSDELKPEQQHPLPSYLEYRHNASIRVYQTNYFASKCAENPNSNSKSFNIKLGAEM 1552	DYHLYPHGPGLNPNAST 2202	ESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKPLYSDTFFSLPITTE 1612.
 1288 TP	632 SR(1406 Sİ	745 SD' . : 1463 NS	802 TK	1521 ALI			905 TV :: 1626 SI	957 HV	: 1671 NG	1011	1730 AF	1062 KI		1121 NPI 1849 PK			1236 RK	1968 TD	1283	2028 YE	1338 DSI	2070 NO	1398 EF	2112 PF	1441 TI	2156 TA	1493 RE	2186	1553 ES
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Ωp	2203GQEALSQTTISWAPPQDTSEYIISCHPVGTD 2233	2233
ò	ro .	1654
QQ	2234 EEPLQFKVPGTSTSATLTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNBGLNQPT 2293	2293
δ	1655 ARLSIRRDRPLSV-HLNLGQKGNRKTSCPIKINQFEGHFMKLQADS	1699
QQ	2294 DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCDSSRWCHDNGV 2347	2347
ò	ALLPENRGKNRYNNILPYDATRVKLSNVDDDPCSDYIN	1759
qq	2348 NYKIGEKWDRQGENGQMMSCTCLGNGKGEPKCDPHEATCYD-DG 2390	2390
ò	1760 ASYIPGNNFREYI 1773	
QQ	2391 KTYHVGEQWQKEXL 2404	

Search completed: March 10, 2006, 19:07:52 Job time : 50.3095 secs

IIII2 Kade Blank (nebto)

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 10, 2006, 18:27:04; Search time 48.7073 Seconds (without alignments)
3944.887 Million cell updates/sec

Title: Perfect score:

US-10-633-742-2 10483 1 MLSHGAGLALWITLSLLQTG......PPIYENVNPEYHRDPVYSRH 1997 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80: * 1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	HPTP beta-like tyr	protein-tyrosine-p	protein-tyrosine-p	hypothetical prote	protein-tyrosine-p	. protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	leukocyte antigen-	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	leukocyte antigen-	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	receptor tyrosine	leucocyte common a	protein-tyrosine-p	protein-tyrosine-p
SUMMARIES	ΙD	\$12050	S17671	D41214	C41214	B49502	A49502	138670	S68700	A55148	T14328	T21913	A57064	A53661	S60613	A49724	JC7503	S46216	A56178	C54689	D54689	TDHULK	TDFFLK	149372	S50893	S68250	T30938	A56493	846217	158148
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	Query. Match Length	1997	583	1557	1630	1615	1767	1337	1238	1111	2302	1367	1188	1187	1216	1118	1226	1898	1912	1894	1691	1897	2029	405	1907	405	2051	1290	1863	1501
di	Query. Match	100.0	26.8	14.6	14.6	14.1	14.1	11.9	11.9	11.4	10.5	9.0	8.7	8.7	8.6	8.5	8.4	8.0	7.9	7.9	7.9	7.9	7.6	7.4	7.4	7.4	7.4	7.3	7.3	7.1
	Score	10483	2807	1530	1526	1475.5	1475.5	1249	1243.5	1198	1097	939	913.5	908.5	906.5	988	877	836	832.5	832	829	826	799.5	780.5	778.5	777	116	168	763.5	748.5
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protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	probable protein-t	protein-tyrosine-p	protein-tyrosine-p	probable protein-t	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	probable tenascin	protein-tyrosine-p	fibronectin precur	protein-tyrosine-p	leukocyte common a	protein-tyrosine-p
150212	B48758	A48758	T31093	S17670	S17669	T19121	JC6312	A48066	A46151	T09070	A48148	S14428	A41622	TDRTLT	T42636
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1499	1262	1496	1437	1452	1452	1585	1440	1457	2314	4006	1445	2477	1301	1273	1422
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7.1		7.1	6.9	6.9	6.9	6.8	6.8	9.9						6.3	6.2

ALIGNMENTS

_	RESULT 1
	protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - numan
	Cisperies: Homo sapiens (man)
	Cidate: 10-Sepi-1994 Haddende Tevtsion 10-Sep-1999 #text_cnange 09-001-2004 Ciacceasion: S12050: S15819: S15819
	R;Krueger, N.X.; Streuli, M.; Saito, H.
	ЕМВО J. 9, 3241-3252, 1990
_	A, Title: Structural diversity and evolution of human receptor-like protein tyrosine phos
	A; Reference number: S12049; MUID:91006018; PMID:2170109
_	A.ACCESSION: \$12050
	A SECTION TO THE TOTAL TO THE TOTAL
	A MOLECULE CYPE: INKNA A DOG AND CONTROL OF THE CYPE:
	A.Cross-references: UNIPROT: P23467; UNIPARC: UP10000034765; GB:X54131; NID: 935787; PIDN:C
	R;de Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.
	FEBS Lett. 282, 285-288, 1991
	A; Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.
	A;Kerencen number: S15010; MU1D:91243813; FM1D:1545282
	A.Ancression: oldsold with concentual translation
	A:MOJecuje tvoe: mRNA
	A.Residues: 1872-1911.'VHMVLOK' <vri></vri>
	A; Cross-references: UNIPARC: UP10000173861
	A;Accession: S15819
	A;Status: not compared with conceptual translation
_	A;Molecule type: mRNA
	A;Residues: 1872-1997 <vr2></vr2>
	A;Cross-references: UNIPARC:UP10000173861
	C; Genetics:
_	A;Gene: GDB:PTPRB; PTPB
_	A,Cross-references: GDB:127352; OMIM:176882
	A; Map position: 12q15-12q21
	C.Keywords: alternative splicing; phosphoprotein; phosphoric monoester nydrolase; recepting
	7:11-24/Domain: signal seddence facatus predicted saios 7:11-34/Domain: signal seddence facatus predicted saios
	F;1626-1642/Domain: transmembrane #status predicted <tmn></tmn>
	F;1643-1997/Domain: intracellular #status predicted <int></int>
	F;1727,1952/Domain: protein-tyrosine-phosphatase homology <ptp></ptp>
-	F,1904/Active site: Cys (phosphocysteine intermediate) #status predicted
	F;1910/Binding site: substrate phosphate (Arg) #status predicted
	100.0%;
	Best Local Similarity 100.0%; Pred. No. 0; Matches 1997; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	OV THE STATE OF TH
	Db 1 MLSHGAGLALWITLSLLQTGLAEPERCNFTLAESKASSHSVSIQWRILGSPCNFSLIYSS 60
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1141 1201 1201 1261 1321 1321 1381 1441	Db 1441 TITMIDRPPPPPPHIR Qy 1501 LKPEQQHPLPSYLEYR Db 1561 PTQQKFCDGPLKPHTA OY 1561 PTQQKFCDGPLKPHTA OY 1621 BCVSAGLFLIGMLVAV OY 1621 BCVSAGLFLIGMLVAV OY 1621 BCVSAGLFLIGMLVAV OY 1621 COVSAGLFLIGMLVAV OY 1621 COVSAGLFLIGMLVAV OY 1631 CPIKINQPEGHFWKLQ OY 1631 CPIKINQPEGHFWKLQ OY 1631 CPIKINQPEGHFWKLQ OY 1631 CPIKINQPEGHFWKLQ OY 1631 CPIKINQPEGHFWKLQ OY 1631 CPIKINQPEGHFWKLQ OY 1631 CPIKINQPEGHFWKLQ OY 1631 CPIKINQPEGHFWKLQ OY 1631 CPIKINQPEGHFWKLQ OY 1741 ATRVKLSNVDDDPCSD	Oy 1801 VTQCVEKGRVKCDHYW Db 1801 VTQCVEKGRVKCDHYW OY 1861 RHFHYTWPDHGVPET Db 1861 RHFHYTWPDHGVPET OY 1921 LQQLDSKDSVDIYGAV Db 1921 LQQLDSKDSVDIYGAV OY 1921 YENVNPEYHRDPVYSR Db 1981 YENVNPEYHRDPVYSR	RESULT 2 S17671 protein-tyrosine-phosphatase (C;Date: 22-Nov-1993 #sequence_C;Accession: S17671; S40287 R;Gebbink, M.F.B.G.; van Etter EES Lett. 290, 123-130, 1991 A.Title: Cloning, expression a A;Reference number: S17669; MU A;Accession: S17671 A;Status: nucleic acid sequenc A;Molecule type: mRNA
61 DTI 61 DTI 121 EKT 121 EKT 181 IAN 241 IIA 301 GSI 361 VSE		661 721 721 781 781 841 901	961 HTFHRLEAGEOYQIMIASVSGSLKNQINVYGRTVPASVQGVIADNAYSSYSLIVSWQKAA 1020
6 B 6 B 6 B 6 B 6	6 B 6 B 6 B 6 B 6 B 7	8 6 8 6 8 6 8	6 8 6 8 6 6 6

1260 BEVEFSRKLEKEKSLINIMMLVDHKRYLVSIKVQSAGMTSEVVEDS 1440 RVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVREADGSDE 1500 1320 RHNASIRVYQTNYFASKCAENPNSNSKSFNIKLGAEMESLGGKRD 1560 AAKISIRAFTQLFDEDLKEFTKPLYSDTPFSLPITTESBPLFGAI 1620 4 VYALLICRQKVSHGRERPSARLSIRRDRPLSVHLNLGQKGNRKTS 1680 TTTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRI 1920 VHDLRLHRVIMVQTECQYVYLHQCVRDVLRARKLRSEQENPLFPI 1980 SLAITWKGPPDWTDYNDFELOWLPRDALTVFNPYNNRKSEGRIVY 1320 OADSNYLLSKEYEELKDVGRNQSCDIALLPENRGKNRYNNILPYD 1740 DYINASYIPGNNFRREYIVTQGPLPGTKDDFWKMVWEQNVHNIVM 1800 KKENWKDKDLTEWRFQGLVPGRKYVLWVVTHSGDLSNKVTAESRTA SRH 1997 1997 (EC 3.1.3.48), receptor type beta - mouse (fragment) se mouse) _revision 15-Mar-1996 #text_change 31-Dec-2004

and chromosomal localization of a new putative receptor-like dUD:92008644; PMID:1655529 nn, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.;

ice not shown; translation not shown

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A;Cross-references: FlyBase:FBgn0004370
C;Superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repe
C;Superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repe
C;Reywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept.
F;1197-1213/Domain: transmembrane #status predicted <TNN>
F;1214-1557/Domain: intracellular #status predicted <INT>
F;125-1515/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1467/Active site: Cys (phosphocysteine intermediate) #status predicted
                                                                                                                                                                                                                                                        A;Residues: 1-904,'L',906-1125,'Q',1126-1165,'YR',1168-1171,'A',1173-1215,'L',1217-1456,
A;Cross-references: UNIPARC:UP1000002B1D9; GB:M80538; NID:g158644; PIDN:AAA28952.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAFKIKVLG----LSEASSSYNRIFQVNDNIFQHSVKELIPGATYQVQAYTIYDGKESVA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 FDRDFITSNSFRVLWEAPKGISEFDKYQVSVATTRRQSTVPRSNEPVAFSDFR---DIAE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGSLYSVVVTTVSGGISSRQVVVEGRTVPSSVSGVTVNNSGRNDYLSVSWLVAPGDV-DN 673
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                                                  A;Cross-references: UNIPROT:P35992; UNIPARC:UPI0000177055; GB:M80465
R;Tian, S.S.; Tsoulfas, P.; Zinn, K.
Cell 67, 675-685, 1991
A;Title: Three receptor-linked protein-tyrosine phosphatases are selectively A;Reference number: A41215; MUD:92034989; PMID:1657402
A;Accession: A41215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 YISRNFITKPNIPGKFI------VWFRNBTILLVLWQPPYPAGIYTHYKVSIEPPDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 DSVLYVEKEGEPPGPAQAAFKGLVPGRAYNISVQTMSEDEISLPTTAQYRTVPLRPLAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYOLSKATTRIRLKROKAVPOHRWIWSLAFLAAFTLKDVRCADLAISIPNNPGLDDGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1467/Active site: Cys (phosphocysteine intermediate) #status predicted F;1473/Binding site: substrate phosphate (Arg) #status predicted
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EQYEVLYSRNGTSDLR----
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                                                                                                                                                                                                                                   A; Molecule type: mRNA
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                    A.Cross-references: UNIPROT:064497; UNIPARC:UPI000017705E; EMBL:X58289
R.Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A.Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
A.Reference number: S40280
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A.Residues: 377-483.
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C;Species: B-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C;Accession: D41214; A41215
R;Yang, X.; Seow, K.T.; Bahri, S.M.; Oon, S.H.; Chia, W.
Cell 67, 661-673, 1991
A;Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in A;Reference number: A41214; MUID:92034988; PMID:1657401
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à	1187 IDSLWFNWSPASGDFDFYELILYNPNGTKKENWKDKDLTEWRFQGLVPGRKYVL 1240	447
qq	786 RDITLSYTPTPQSSSKFDIYRFSSGDAEIRDKEKLANDTDRKVTFTGLVPGRLYNI 842	0.0
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à	1410 LNIMMLVPHKRYLVSIKVQSA-GMTSEVVEDSTITMIDRPPPPPHIRVNEKDVLIŞKŞS 1468	අ
ą	1017 GVIKNLKPGETYVFKIQAKTAIGFGPEREYRQTMPILAPPRPATQVVPTEVYRSSST 1073	රි ස්
à	1469 INFTUNCSMFSDINGAVKYFTVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQIN- 1527	3 8
Q	1074 İQIRFRKNYFSDQNGQVRMYTIIVAEDDAKNASGLEMÈSWLDVQSYSVWLPYAIDP 1129	: A
à	1528 YFASKCAENPNSNSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQL 1587	ð
a a	YYPPENRSVEDFTIGTENCDNHKIGYCNGPLKSGTTIGVKVRRFT	q
ጵ ዳ	1588 FDEDLKEFTKPLYSOTFFSLPITTESEPLFGAIEGYSAGIFLIGMLVAVVALLICKOKVS 1647 1	ò
λ	HGRE-RPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKE	පු .
ą	1224 NCRKITKDSRANDNMSLPDSVIEQNRPILIKNFAEHYRLMSADSDFRFSEE 1274	કે ક
λ	1707 YEELKDVGRNQSCDIALLPENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGN 1766 : :	3 8
ą	1275 FÉELKHVGRDÓPCTFADLÞCNRPKNRFTNILÞÝDHSRFKLQPVDDDEGSDÝINANKVÞGH 1334	; 음
À	1767 NFRREYIVTQGPLPGTKDDFWKAVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYG 1826	ò
ą.		ą d
ጵ ብ	1827 DLILQMLSESULPERTIREKIC-GEEQLDAHRLIRHFYTVWPHGVPETTQSLIQFVR 1885	ờ
ά	1886 TVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVH 1945	අ
ą		∂ £

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tein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 10D, long splice form precurso species: Drosophila melanogaster bate: 28-May-1992 #sequence_revision 12-Jun-1992 #text_change 24-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: C41214

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: FlyBase:Ptp10D
Cross-references: FlyBase:Pbgn0004370
Cross-references: FlyBase:Pbgn0004370
Cross-references: FlyBase:Pbgn0004370
Cross-references: FlyBase:Pbgn0004370
Superfamily: protein-typosine-phosphatase, receptor type 4E; fibronectin type III repeated to the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the conte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 SYRLDYS-PPFGYPEPNTTIA-----SREIG---DEIQFSRALPGTKYNFWLYYTNFT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 YISRNFTTKPNTPGKFI------VWFRNETTLLVLWQPPYPAGIYTHYKVSIEPPDAN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 PGKTFNVIVKTVSGKVTSWPATGDVTLRPLPVRNLRSINDDKTNTMIITWEADPASTQDE 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 HHDWLTWTTT-----TAPDPPSNLSVQVRSG--KNAILLWSPPTQGSY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 EQYRILLFNDSVVLLNITVGKEETQYVMDDT-----GLVPGRQYEVE-----VI 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 VESGNIKNSERCOGRIVPLAVIQLRVKHANETSLSIMWQT--PVAEWEKYIISL----AD 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 RDLLLIHKSLSKDA-KEFTFTDLVPGRKYMATVTSISGD-LKNSSSVKGRTVPAQVTDLH 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562 VANQGMTSSLF-TNWTQAQGDVEF--YQVLLI----HENVVIKNESISSETSRYSFHSLK 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              615 SGSLYSVVVTTVSGGISSROVVVEGRTVPSSVSGVTVNNSGRNDYLSVSWLVAPGDV-DN 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      674 YEVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTITTRSGKYENHSFSQERTVPDK 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VIVSCVSGELSAQKMAVGRIFPDKVANLEAN-NNGRMRSLVVSWSPPA-GDW 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LYQLSKATTRIRLKRQKAVPQHRWLWSLAFLAAFTLKDVRCADLAISIPNNPGLDDGA-- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          734 VOGVSVSNSARSDYLRVSWVHATGDFDHYEVTIKNKNNFIQTKSIPKSENECVFVQLVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duery Match
14.6%; Score 1526; DB 2; Length 1630;
Sest Local Similarity 27.7%; Pred. No. 1.5e-76;
fatches 508; Conservative 271; Mismatches 640; Indels 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 SLKVKWORPPGNVDSYNITLSHKGTIKESRVLAPWITETHFKELVPGRLYQ--
folecule type: mRNA
tesidues: 1-1630 <YAN>
:ross-references: UNIPARC:UP10000177054; GB:M80465
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-----LLPG 469

---DRTRFTLES----

Š	794 RI.YSVTVTVTKSGOYEANEOG-	YEANEOGNGRTT PEPUKDI.TI.RNRSTEDI.HVTW-SGANGDV 846	& 	183
3 A		FVVTRPSSPITEDLKSIRMGLNISWKSDVNSKO 52	qa —	13
Š		OYKILVLTISGDVOOSA 89	<i>&</i>	18
. A			qa	
ò	900 FIEGFTVPSAVK	FIEGFTVPSAVKNIHISPNGATDSLTVNWT-PGGGDVDSYTVŞAFRHSQKVDSQTIPKHV 958	<i>&</i> 	
đ	: : : : 577 YFQA-VYPNPPR	::	q a	15(
è	959 FEHTFHRLEAGE	FEHTFHRLEAGEQYQIMIASVSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQK 1018	RE	RESULT 5
Ob	623B		i d	protein-tyre
ò	1019 AAGVAERYDILL	CKKIO		Species: Date: 10-1
ą	633	:	, K	Accession Oon, S.H.
ò	1079 TEGRIVPAAVID	TEGRIVPAAVIDLRITENSTRHLSFRWTASEGELSWYNIFLYNPDGNLOERAQ 1131	- A A	Title: Alt
Q	666 EVNTTVPPNPVS	EVNTTVPPNPVSNIIQLVDSRNITLEMPKPEGRVESYILKWWPSDNPGRVQTKNVSENKS 725	444	Accession Molecule
È	1132 VDPL-VQSFSFQ	VDPL-VQSFSFQNLLQGRMYKMVIVTHS-GELSNESFIFGRTVPASVSHLRGSNRNT 1186	44	Residues: Cross-ref
qa	726 ADDLSTVRVLIG	ADDLSTVRVLIGELMPGVQYKFDIQTTSYGILSGITSLYPRIMPLIQSDVVVANGEKEDE 785		Genetics:
È	1187 TDSLWFNWSP	TDSLWFNWSPASGDFDFYELILYNPNGTKKENWKDKDLTFWRFQGLVPGRKYVL 1240	44	A; Cross-refe
Op	786 RDTITLSYTPTP	RDTITLSYTPTPQSSSKFDIYRFSSGDAEIRDKEKLANDTDRKVTFTGLVPGRLYNI 842	00	Superfami
ò	1241 WVVTHSGDLSN-	WVVTHSGDLSN-KVTAESRTAPSPPSLMSFADIANTSLAITWKGPPDWTDYNDFELQWLP 1299	<u>Б.</u> Б.	1254-1270
qq	843 TVWTVSGGVASL	RWDLPKGEYN	Ca. Ca	1353-1573
ò	1300 RDALTVFNPYNN	RDALTVFNPYNNRKSEGRI-VYGLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTK 1354	i Di	1531/Bind
QQ	901 ADNLLAQN	ADNLLAQMMTTRNEITISDLÄPHRNYTÄTVVVRSGTESSVLRSSSPLSASFTINEA 956		Query Mate
ò	1355 -PDKIQNLHCRP	-PDKIQNLHCRPQNSTALACSWIPPDSDFDGYSIECRKWDTQEVEFSRKLEKKSL 1409		
рр	957 VPGRVERFHPTD	VPGRVERFHPTDVQPSBINFBWSLPSSEANGVIRQPSIAYTNINNLTDAGWQDFBSBEAF 1016	Š	iń
È	1410 LNIMMLVPHKRY	LNIMMLVPHKRYLVSIKVQSA-GMTSEVVEDSTITMIDRPPPPPPHHIRVNEKDVLISKSS 1468	du	H
qq	1017 GVIKNLKPGETY	GVIKNLKPGETYVFKIQAKTAIGFGPEREYRQTMPILAPPRPATQVVPTEVYRSSST 1073	ò	in
ò	1469 INFTVNCSWFSD	INFTVNCSWFSDTNGAVKYFTVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQTN- 1527	9 0	H
DP .	1074 IQIRFRKNYFSD	IQIRFRKNYFSDQNGQVRMYTIIVAEDDAKNASGLEMPSWLDVQSYSVWLPYAIDP 1129	8	
ò	1528 YFASKCAENPNS	YFASKCAENPNSNSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQL 1587	qa —	.23
qq	1130 YYPFE	PPENRSVEDFTIGTENCDNHKIGYCNGPLKSGTTIGVKVRRFT 1174	ò	9
È	1588 FDEDLKEFTKPL	FDEDLKEFTKPLYSDTFFSLPITTESEPLFGAIBGVSAGLFLIGMLVAVVALLICRQKVS 1647	qa	23
.· g	1175GADKFT	DTAYSFPIQTDQDNT-SLIVAITVPLTIILVLLVTLIFYKRRN 1223	8	
ò	1648 HGRE-RPSARLS	HGRE-RPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFMKLQADSNYLLSKE 1706	qa	Ë
qq	: : : : 1224 NCRKTTKDSRAN		ò	7
ò	1707 YEELKDVGRNQS	YEELKDVGRNGSCDIALLPENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGN 1766	oda .	4
qa	1275 FEELKHVGRDQP	FEBLKHYGRDQPCTFADLPCNRPKNRFTNILDYDHSRFKLQPVDDDGGSDXINANYVPGH 1334	ò	ďs
&	1767 NFRREYIVTOGP	NFRREYIVTQGPLPGTKDDFWKMVWEQNVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYG 1826	qa	4
QQ	1335 NSPREFIVTQGP	NSPREFIVIQGPLHSTRDDFWRMCWESNSRAIVMLTRCFEKGREKCDQYWPNDTVPVFYG 1394	ò	ō .
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		· 八樓子 · 小花的		j
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C;Species: Drosophila melanogater
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: B49502
R;Oon, S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 268, 23964-23971, 1993
A;Title: Alternative splicing in a novel tyrosine phosphatase gene (DPTP4E) of Drosophil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repe C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept E;1254-1270/Domain: transmembrane #status predicted <TWN>
F;1271-1615/Domain: intracellular #status predicted <IWN>
F;1373-1573/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1352-1573/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1525/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1531/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                    protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type 4E, splice form B precursor
                        TVRDYINRSPGAGPTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVH 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 KDIKFSRALPGTEYNFWLYYTNSTHREQLTWTVNITTAPDPPANLSVQLRSSKSAFITWR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691 AK----SVRECSFSSLTPGRLYTVTITTRSGKYENHSFS-----QERTVPDKVQGVSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 EREGEPPGPAQAAFKGLVPGREYNISVQTVS---EDETSSVPTTARYLTVPERVLNVTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             633 RQVVVEGRITVPSSVSGVTVNNSGRNDYLSVSWL--VAPGDVDNYEVTLSHDGKVVQSLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          741 NS-ARSDYLRVSW--VHATGDFDHYEVTIKONONFIQTKSIPKSEN-ECVFVQ----LVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 EAYTTSSSFRVRWEPPRTYSEFDAYQVMLSTSRRIF---NVPRAANGDSVYFDYSDILEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  793 GRLYSVTVTTKSGQYEANEQGNGRII-PEPVKDL--TLRNRSTEDLHVTWSGA-NGDVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 KEFTFTDLVPGRKY--MATVTSISGDLKNSSSVKGRTVPAQVTDLHVANQGMTSSLFTNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQAQGDVEFYQVLLIHENVVIKNESIS---SETSRYSFHSLKSGSLYSVVTTVSGGISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 PPGSGRYSGFRIRVLGLTDLPFERSYSLEGNETLQLSAKELTPGGSYQVQAYSVYQGKES
DLILOMLSESVLPEWTIREFKIC-GEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.1%; Score 1475.5; DB 2; Length 1615; Best Local Similarity 29.3%; Pred. No. 9.6e-74; Matches 455; Conservative 257; Mismatches 662; Indels 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-1615 <CON>
A;Cross-references: UNIPROT:Q9W4F5; UNIPARC:UPI0000177053; GB:L20894
C;Genetics:
                                                                                                                                                                                                                  1509 MVQTEQQYICIHQCLLAVLEGK-----ENIVGPARE 1539
                                                                                                                                                                                       1946 MVQTECQYVYLHQCVRDVLRARKLRSEQENPLFPIYE 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: FlyBase:Ptp4E
A;Cross-references: FlyBase:FBgn0004368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B49502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 1605/3
  1827
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466 YRISYHEQTNASEVPAPPPVAAESQITTNLTEYTLDSLLAGRRYLIAVQALSKGVASNAS 525

849 YEIQL--LFNDMKVFPPF-----HLVNTATEYRFTSLTPGRQYKILVLTISGDVQQSAF

901 -IEGFTVPSA--VKNIHISPNGAIDSLTVNWTPGGGDV----DSYTVSAFRHSOKVDSQT

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1285 PDWTDYNDFELQWLPRDALTVFNPYNNRKSEGRIVYGLRPGRSYQFNVKTVSGDSWKT-- 1342
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                                                                                                                                        IVSWQKAAGVAERYDILLLTENGILLRNTSEP-----ATTKQHKFEDLTPGKKYKIQIL 1066
                                                                                                                                                                                                                                   TVSGGLFSKEAQTEGRTVPAAVTDLRITENSTRHLSFRWTASEGELSWYNIFLYNPDGNL 1126
                                                                                                                                                                                                                                                                                                                            QERAQVDPLVQ-----SPSFQNLLQGRMYKM-VIVTHSGELSNESFIFGRTVP--- 1173
                                                                                                                                                                                                                                                                                                                                                                                                                       ----ASVSHLRGSNRNTTDSLWFNWSPASGD---FDFYELILYNPNGTKKENWKDKDLT 1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              982 ADVSVSTLMRSSAPISAŠYQTLTAPPGKVDYFQPSDVQPGEVTFEWSLEPAEQHGPIDYF 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQHPLPSYLEYRHNASIRVYQTNYFASKCAE--NP----NSNSKSFNIKLGAEMESLG-G 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IASGLEMPSWQDVQAY-TVWLPYQAIEPYNPFLTSNGSRKS---SLEAEHLTIGTA 1204
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                                                                                                                                                                                                                                                              DITRYTRPAAPLIQELRSIDQG----LMLSWR---SDVNSRQDRYEVHYQRNGTR-EERT
                                             IPKHVFEHTFHRLEAGEQYQIMIASVSGSLKNQINVVGRTV-PASVQGVIADNAYSSYSL
                                                                       |: | : | : | . | . | . | SDVFIANAGHEGGQDETIT----LSYTPTPADSTRFDIYRFSMGDPTIXDKEKLANDTER
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A Cross-references: PlyBase:FBgn0004368
C;Superfamily: fibronectin type III repeat homology; protein-tyrosine-phosphatase homolog.
C;Superfamily: fibronectin type III repeat homology; protein-tyrosine-phosphatase homolog.
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptc F;1254-1270/Domain: transmembrane #status predicted <TWN>
F;1271-1767/Domain: intracellular #status predicted <INT>
F;1353-1573/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1555/Active site: Cys (phosphocysteine intamediate) #status predicted
F;1531/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                             Drosophil
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 4E, splice form A precursor
                                                                                                                                                                                                                                                                    GB:L20894
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                      Species: Drosophila melanogaster
Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
                                                                                                                                             (DPTP4E)
                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:09W4F5; UNIPROT:024495; UNIPARC:UPI0000177052; A;Note: authors translated the codon ATA for residue 1715 as Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPGSGRYSGFRIRVLGLTDLPFERSYSLEGNETLQLSAKELTPGGSYQVQAYSVYQGKES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
14.1%; Score 1475.5; DB 2; Length 1767;
Best Local Similarity 29.3%; Pred. No. 1.1e-73;
Matches 455; Conservative 257; Mismatches 662; Indels 180;
                                                               C,Accession: A49502
R,Oon, S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 268, 23964-23971, 1993
A,Fitle: Alternative splicing in a novel tyrosine phosphatase gene A,Reference number: A49502; MUID:94043220; PMID:8226938
                                                                                                                                                                                           A;Accession: A49502
A;Molecule type: mRNA
A;Residues: 1-1767 <OON>
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QERAQVDPLVQ-----SPSPQNLLQGRMYKM-VIVTHSGELSNESFIFGRTVP--- 1173
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TVSFGVESPHPLELNVTMPPQPVSNVVPLVDSRNLTLEWPRPDGHVDFYTLKWWPTDE- 747
                                                                                                                                          EDRVEFKNVTQLEDLSSPSVRIPIEDLSPGRQYRFEVQASSNGIRSGTHLSTRIMPLIQ 807
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                                                                                                                                                                                                                                       ----ASVSHLRGSNRNTTDSLWFNWSPASGD---FDFYELILYNPNGTKKENWKDKDLT
                                                                                                                                                                                                                                                                              808 SDVFIANAGHEQGQDETIT----LSYTPTPADSTRPDIYRFSMGDPTIKDKEKLANDTER
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RESULT 7
138670
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human
N;Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 09-Jul-2004
C;Accession: 138670; 152599
R;Ostman, A; Yang, Q; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994

GVAE---RYDILLLTENGILLRNTSEPATTKQHKFEDLTPGKK----YKIQILTVSGGLF 1073

. 5. A. C.

Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
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Molecule type: MN ŭ PID 501,525,536,582,603,6 enhanced novel A;Molecule type: mRNA A;Residues: 1-1337 <RES> A;Cross-references: UNIPROT:Q12913; UNIPARC:UPI000017383B; EMBL:U10886; NID:g558754; ۵ 61; 700 FHRLEAGEQYQIMIAS -- VSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAA 1020 Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is Reference number: 138670; MUID:95024024; PMID:7937872 141 849 246 962 804 E--ELTODSRL------QVNISDLKPGVQYNINPYLLQSNKTKGDPLAQKVAW-- 291 LVGLEPGTRYNATVYSQAANGTEGQPQAIEFRTNAIQVFDVTAVN-ISATSLTLIWKVSD 390 SLTPGRLYTVTITTRSGKYENHSFSQE---RTVPDKV---QGVSVSNSARSDYLRVSWVH 754 97 Title: Molecular cloning, characterization, and chromosomal localization of Reference number: IS2599; MUID:95086212; PMID:7994032 755 ATGDFDHYEVTIKONONFIQTKSIPKSENE------CVFVQLVPGRLYSVTVTTKS EIQLLFNDMKVFPPFHLVNTATEYRFTSLTPGRQYKILVLTI-----SGD--VQQSAFIE TVPSSVSGVTVNNSGRNDYLSVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFS G----NETWGDPRVIKVITEPIPVSDLRVAHGCEEGCSLSWSNGNGTASCRVLLESIGSH GFTVPSAVKNIHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSOKVDSQTIPKHVFEHT TVATGENGITQISSTAESFHKQNGTGTP----QVETNTSEDG---ESSGANDSLR----F;1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP> ?Ty2,82,93,9104,142,112,121,231,288,278,342,351,376,391,365,413,431,501,55 F;1239/Active site: Cys (phosphocysteine intermediate) #status predicted F;1245/Binding site: substrate phosphate (Arg) #status predicted DB 1; Length 1337, <PTP> %; Pred. No. 3e-61; 215; Mismatches 547; Indels GOYEANEQ-GNGRTI----PEPVKDLTLRNRSTEDLHVTWSGANG Y.; Hirai, J.; Yazaki, 11.9%; Score 1249; ilarity 28.9%; Pred. No. 3e Conservative 215; Mismatche ;Cross-references: GDB:385040; OMIM:600925; Map position: 19q13.4-19q13.4 Honda, H.; Inazawa, J.; Nishida, lood 84, 4186-4194, 1994 A; Experimental source: HeLa Query Match Best Local Similarity Matches 417; Conserv Accession: I52599 Gene: GDB: PTPRJ 247 641 20 107 805 191 850 903 Function: 셤 g g 8 용 ઠે g 8 셤 8 셤 ઠે ò ò

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FNWSPASGDFDF-YELILYNPNGTKKENWKDKDLTEWRFQGLVPGRKYYLWV---VTHSG 1247
                                                                                                                                                                                                                                                                                              IQNLHCR-PQNSTAIACSWIPPDSDFDGYSIE-----CRKMDTQEVEFSRKLEKEKS 1408
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                                                                                       PLVQSFSFQNLLQGRMYKMVIVTH--SGELSNESFIFGRTVPASVSHLRGSNRNTTDSLW 1191
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391 NESSSNYTYKIHVAGETDSSNLMVSEPRA-----VIPGLRSSTPYNITVCPVLGDIE 442
                                                      CTPGFLQVHTPPVPVSDFRVTVVSTTEIGLAMSSHDAESFQMHI---TQEGAGNSRVEI- 498
                                                                                                                                                       782 YLNF----STSYNISITTVSCGKMAAPTRNICITGITDPPPPDGSPNI-----TSVSH 830
                                                                                                               TINOSIIIGGLFPGTKYCFEIVPKGPNGTEGASRIVCNRIVPSAVFDIHVVYVITTE-MW 557
                                                                                                                                                                                                                                                             TYVTYLIRTEEKGRSQSLSEVLKYEIDVGNESTTLG-----YYNGKLEPLGSYRAC 931
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                                                                                                                                                                                                           GDPNSTAQYTR-----PSNVSNIDVSTNTTAATL----SWQNFDDASPTY---SYCLLIE
                                                                                                                                                                                                                                             PYNNRKSEGRIVYG------LRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDK
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C;Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repeat C;Reywords: phosphoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;29-1238/Porduct: HPPP beta-like tyrosine phosphatase #status predicted <MAT>
F;29-1238/Porduct: HPPP beta-like tyrosine phosphatase homology <3FR>
F;26-347/Domain: fibronectin type III repeat homology <PTP>
F;56-1388/Domain: protein-tyrosine-phosphatase homology <PTP>
F;1146/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1146/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                               PIDN
                                                                                                                                  a murine receptor-type tyrosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157
                                                              C;Accession: S68700
R;Kuramochi, S.; Matsuda, S.; Matsuda, Y.; Saitoh, T.; Ohsugi, M.; Yamamoto, FEBS Lett., 378, 7-14, 1996
A;Title: Molecular cloning and characterization of Byp, a murine receptor-tyle; A;Reference number: S68700; MUID:96140699; PMID:8549806
A;Accession: S68700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       750 VSWVHATGDFDHYEVTIKNKNNFIQTKSIPKSENECVFVQLVPGRLYS----VTVTTKSGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----THSSVNISGLKPGTN-NTFAFPESNET-QADFAVAEEVPDANGTKRIPVTNLSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FHLVNTATEYRFISLTPGRQYKILVLTISGDVQQSAFIEGFTVPSA--VKNIHIS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q64455; UNIPARC:UP100000013C2; GB:D45212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPTP beta-like tyrosine phosphatase precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA
A;Residues: 1-1238 <KUR>
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Mon

Oy 1345	S KPIFGSVRTKPDKIQNLHCR-PQNSTAIACSWIPPDSDFDGYSIECRKMDTQ 1395
Db 610	O VPGWINFCTEPEPVISFHCEVVPKEPALVLKWACPFGWYIGFELGVRSDSWDNMTRLENC 669
Qy 1396	S EVEFSRKLEKEKSLLNIMMLVPHKRYLVSIKVQSAGMTSEVVEDSTITMIDRPPPPPP 1453
DP 670	O TSDDDTECRTEVAYLNFSTSYNISIATLSCGRMALPAQNICTTGITDPPTPDGSP 724
-	HIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFTVVVRRADGSDELKPEQQHPLPSYL
	NITSVSHNSVKVKFSGFBASHGPIKAYAVIL/TTGBAAQPSADVLKYTYE 773
Oy 1514 Db 774	4 BYRHAASIRYYOTNYFASKCAENPNSNSKSFNIKLGAEMESLGGKRDPTQQKFCDG 1569 ::: : : : : : : : :
-	PLKPHTAYRISTRAFTOLFDEDIKEFTKPLYSDTPFSLP1TTESEP
Qy 1616	LFGAIEGVSAGLFLIGMLVAVVALLICR
Db 875	GGAVFGCIFGALAITAVGGFIFWRKKRTDAKNNEVSFSQIKP 916
Oy 1673	QKGN
Db 917	7KKSKLIRVENPEAYFKKQQADSNCGFAEEYEDLKLIGISLPKYTAEIAENRGKNR 971
Qy 1733	3 XNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGPLPGTKDDFWKMVWE 1792
Db 972	YNNVLPYDISRVKLS-VQTHSTDDYINANYMPGYHSKKDFIATQGPLPNTLKD
Qy 1793	
Db 1031	KNVYAIVMLTKCVEQGRTKCEEYWPSKQ-AQDYGDITVAMTSEV
Qy 1853	3 QLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVHCSAGVGRTG 1912
Db 1090	NSESHPL-RQFHFTSWPDHGVPDTTDLLINFRYLVRD
Oy 1913	TFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTBCQYVYLHQCVRDVLRARKLRS- 1971
Db 1149	
Oy 1972	2EQENPLFPIYENVNP 1986
Db 1209	DLIYQNTTAMTIY
RESULT 9 A55148 protein-tyrod NyAlternate 1C, Species: RC, C, Accession: R, Mauro, L.J. J, Biol. L.J. J, Richernot A, Reference 1A, Accession: A, Accession:	RESULT 9 A55148 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat N;Alternate names: OST-PTP; osteotesticular protein-tyrosine-phosphatase C;Species: Rattus norvegicus (Norway rat) C;Bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A55148 R;Mauro, L.J.; Olmmeted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E. A;Title: Identification of a hormonally regulated protein tyrosine phosphatase associate A;Fetence number: A55148; MUID:95074080; PMID:7527035 A;Accession: A55148 A;Status: not compared with conceptual translation A;Ratus: not compared with conceptual translation A;Molecule type: mRNA A;Cessidues: 1-1711 **MAUP.**AMUPARC:UPIO00004DCID; GB:Li36884
E	The second secon

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C; Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosing C; Comment: The sequence contains ten fibronectin type III rep C; Superfamily; protein-tyrosine-phosphatase, receptor type OST; fibronectin type III rep C; Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot F; 1-18 Domain: signal sequence #status predicted <SIG. P; 19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <WM P; 1174-1398/Domain: protein-tyrosine-phosphatase homology <PPP1>
F; 1356/Active site: Cys (phosphocysteine intermediate) #status predicted P; 1356/Binding site: substrate phosphate (Arg) #status predicted
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1.4.

1276 STRHLSFRWTASEGELSWYNIFLYNPDGNLQERAQVDPLVQSFSFQNLLQGRMYKMVIVT 1156 219 278 325 812 998 LRNTSE-PATTKOHKFEDLTPGKKYKIQILTVSGGLFSKEAQTEGRTVPAAVTDLRITEN 1096 HSGELSNESFIFGRTVPASVSHLRGSNRNTTDSLWFNWSPASGDFDFYELILYNPNGTKK 1216 LA--ITWKGPPDWTDYNDFELQWLPRDALTVFNPYNNRKSEGRIVYGLR---PGRSYQFN 1331 VKTVSGDSWKTYSKPIFGS-----VRTKPDKIQNLHCRPQNSTAIACSWIPPDSDFDGYS 1386 1387 IEC-RKMDTQEVEFSRKLEKEKSLLNIMMLVPHKRYLVSIKVQSAGMT-SEVVEDSTITM 1444 53 752 383 429 487 978 547 607 812 923 527 100 586 160 644 704 921 | :: | : | | CTPHELKICASAG------PHQIWGPSATEWTYPSYPSDLVLTPLRNELWASW SDLTIAMGPAPGQLEGYKVTWHQDGSQRSPGDLVDLGPDTLSLTLKSLVPGSSYTVSAWA VLLIH--ENVVIKNESISSETSRYSFHSLKSGSLYSVVYTTVSGGISSRQVVVEGRTVPS VHATGDFDHYEVTIKNKNNFIQTKSIPKSENECVFVQLVPGRLYSVTVTTKSGQYEANEQ 326 KAGLGARDGY--VLKLSGPMESTSTLGPEECNAVFPGPLPPGHYTLQLKVLAGPYDAWVE 867 VNT-----ATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEGFTVPSAVKNIHISPNGAT GNISVPSGATHVIFCGLVPGAHYRVDIASSTGDISQS--ISGYTSPLPPQSLEVISRSSP DSLTVNWTPGGGDVDSYTVSAFRH-SQKV--DSQTIPKHVFEHTFHRLEAGEQYQIMIAS VSGSL-KNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAAGVAERYDILLLTENGIL 548 WAGNIGSDSOKIHSCIRPAPPINLSLGFAHQPAALKASWYHPPGGRDAFHLRLYRLRPLT SVSGVTVNNSGRNDYLSVSWLVAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFSSLTP PPDHLALRALGISS-LOAFWNSSEGAISFHLMLIDLLGGINTIAVIRQGVSTHTFLHLSP GRLYTVTITTRSGKYENHSFSQERTVPDKVQGVSVSNSARSDY------LRVSW GN-----GRIIPEPVKDLTLRNRSTEDLHVTW-SGANGDVDQYEIQLLFNDMKVFPPFHL 727 WAGPL-----YPLI--PN---ENWKDKDLTEWRPQGLVPGRKYYLWVVTHSGDLSNKVTAESRTAPSPPSLMSFADIANTS -----AVVNLAWPSGP-LGQGACHAQLS DAGHLSWEQP-----LKLGQELFMLRDLTPGHTISMS HANETSLSIMWQTPVAEWEKYIISLADRDLLLIHKSLSKDAKE------FTFTDLVP HGKSTSLFLSWVAAELGGFDYALSLRSVD----SSGSPEGQQLQAHTNESGFEFHGLVP GRKYMATVTSISGDLKN-SSSVKGRTVPAQVTDLHVANQGMTSSLFTNWTQAQGDVBFYQ 302; Gaps Indels Query Match 11.4%; Score 1198; DB 1; Best Local Similarity 25.3%; Pred. No. 3.1e-58; Matches 411; Conservative 256; Mismatches 657; 979 668 477 46 101 587 161 220 279 753 813 384 922 488 608 1097 1157 1217 1277 781 1332 864 705 749 813 g 음 셤 요 ઠે a à g ઠે 셤 g ઠે 셤 a ઠ 셤 셤 a 요 셤 셤 ò 용 δ ò ठे ઠે ઠે δ ઠે ઠે à 8 8

229 LWSTTSPSPTLGRVTP-TVRTTQSSSTAARSKISSVWKEPISFVVTH 274 69 PTFRIDNTTYGCNLQDLQAGTIYNPKIISLDEERTVVLQTDPLPPARFGVSKE 121	: : : : : : : : : : : : : : : : : : : : : : :		179 YNIAITAVSGGKRSFSVYTNGSTVPSPVKDIGIS-TKANSLLISWSHGSGNVE 230 ::: :	231 RYRLMLMDKGILVHGGVUDKHATSYAFHGLSP- 262 :	263 GYLYNLMEVS 293 :: : : : : 491 SFIYNSHPHNDFPASTRAEEOSSPVVTTRNOYMTDITA-EOLSYVVRRLVPFTEHTISVS 549	NLKVTNDGSLTSLKVKW-QRPPGNVDSYNITLSHKGTIKESRVLAPWITETHF appring/Depting/Depting/Decting/Nuk	KELVPGRLYQVIVSCVSGELSAQKMAVGRTFPDKVANLEANNNGRMRS	605 TIYATELDTNRAFQMTTVDNSFLITGLKKYTRYKMRVAASTHVGESSLSEENDIFVRTPE 664 394LVVSWSPPAGDWEQYRILLFNDSVVLLNITVGKEETQY 431	665 DEPESSPQDVQVTGVSPSELRLKWSPPEKPNGIIIAYEVLYQNADTLFVKNTSTTDI 721	VIDOLINIA PER PARTITION OF THE PROPERTY OF THE	490 PVAEWEKYIISLADRDLLLIHKSLSKDAKEFTFTDLVPGRKYMATVTSISGDLKNSSSVK 549	GRTVPAQVTDLHVANQGMTSSLFTNMTQAQGDVEFYQVLLIHENVVIKNESISSETSRYS	610 FHSLKSGSLYSVVYTTVSG-GISSRQV-VVEGRTVPSSVSGVTVNNNSGRND 658 831EVSASTLKGEGIRSRPISILTEEDAPDSPPQNFSVKQLSGVTV
g &	a ò	. A	& g	S &	& 8	8 8	8 8	임 <i>&</i>	op :	∂ 8	કે ક	ි රි සි	8 4 8 4 8 4 8 4 8 4 8 4 8 8 4 8 8 8 8 8
Qy 1445 IDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKXFTVVV 1492	Qy 1493READGSDELKPEQQHPLPSYLEYRH-NASIRVYQTNYFASKCAENPNSNSKSFNIKLG 1549	MESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDLKEFTKPLYSDTFF	Db 1022 TEDCDNTQE-ICNGRLKSGFQYRFSVVAFSRLNTFBTILAFSAFSBFRASISLA 1074 Qy 1606 SLPITTESEPLFGAIEGVSAGLFLIGMLVAVVALL-ICROKVSHGRERPSARLSIRRDRP 1664 :	Db 1075 IIPLTVMLGAVVGSIVIVCAVLCLLRWRCLKGPRSEKDGFS-KELMP 1120 Qy 1665 LSVHLNLGQKGNRKTSCPIKINQFEGHFWKLQADSNYLLSKEYEELKDVGRNQSCDIALL 1724	Db 1121 YNLWRTHRPIPIHSFRQSYEAKSAHAHQTFFQEFEELKEVGKDQPRLEAEH 1171 OY 1725 PENRGKARYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRREXIVTOGPLPGTKD 1784	: :: :: :: :: :: :: :: ::	1232 DFWRLVWEQOVHVIIMLTVGMENGRVLCEHYWPANSTPVTHGHITIHLLAEBFEDEWTRR	Qy 1845 EFKI-CGEEQLDAHRLIRHFHYTWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPTVVH 1903	OY 1904 CSAGVGRTGTF1ALDR1LQQLDSKDSVD1YGAVHDLRLHRVHMVQTBCQYVYLHQC 1959	1950 CSAGOGRIGIT VALLERLINGLEEEROVALVEN VIILKRINKELAILGILSKIIFLINGSCLILIN 1960PIYEDVLRARKLRSEQENPLFPIYENVNPEYHR	Db 1410 ILEGPPDSSDSGPISVMDFAQACAKRAANANAGFLKEYKLLKQAIKDGTGSLLPPPDYNQ 1469	1470 NSIVSR 147	TESTULT 10 RESTULT 10 RESTULT 10 RESTULT 10 RESTULT 10 Protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type, GMCI precursor - rat C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C.Accession: T14328 R.Wright, M.B.; Hugo, C.; Selfert, R.; Disteche, C.M.; Bowen-Pope, D.F. A.Hitle: Proliferating and migrating mesangial cells responding to injury express a nove A; Reference number: Z17986; MUID:98395110; PMID:9727007 A.Accession: T14328 A.Accession: T14328 A.Accession: T14328 A.Stetus: preliminary; translated from GB/EMBL/DDBJ A.Stetus: preliminary; translated from GB/EMBL/DDBJ A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: preliminary A.Stetus: PROSO C.Steywords: phosphoric monoester hydrolase F.19-2302/Product: protein-tyrosine phosphatase receptor type, GMCI #status predicted C.Steywords: phosphoric monoester hydrolase F.19-2302/Product: protein-tyrosine phosphatase receptor type, GMCI #status predicted C.Duery Match Best Local Similarity A.Steywords: Pred: No. 2.2e-52; Matches 545; Conservative 335; Mismatches 856; Indels 518; Gaps 111; Matches 545; Conservative 335; Mismatches 856; Indels 518; Als Als Als Als Als Als Als Als Als Als

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	1692 FWKLQADSNYLLSKRYEELKDVGRNQSCDIALLPENRGKNRYNNILPYDATRVKLSNVDD 1751 	දු අ
00y 95.	QKVSHGGNRKTSCPIKINQFEGH	දු දු
Oy 86	DEDLEGE INCLESSION FOR THE SERVICE GARDON SANGE THE TRANSPORT OF THE SERVICE STREET SERVICES	e 6
.t	NPPCIEGKTKFSGNEEI YVI GADNACMI PGNEEKI CNGPLKPKKQYLFKFRA	a a
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` `	RAPICYYNDDHGPIRNVQVLVAETGAQQDGNVTKWYDAYFNKA-RPYFTNEGFP 182	8 8
q ₀	TVNCSWESDTNGSVKYFTVXVRRADGSDRIKEPEDDID BSVI RVBHNÅSTRVVOTNVP	3 2
, vo	1417 PHKRYLVSI-KVQSAGMTSEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINF 1471 11717 GGHTYNISVAINSAGAGRKVOMRITMDIKABARPKSKEIPIRDATGKLIVTSTITTI 1774	<b>&amp;</b> &
Query Matc Best Loca Matches	1366 QNSTAIACSWIPPDSDFDGXSIECKKWDIQEKEFSKKLEKEKSLANIMW-LV 1916 	e 5
A, Map posit A, Introns:	KTTEINNLEVFTRYSVVITAFVGNVSRAYTDGKSSAEVIITTLESVPKDPPNNMTFQKIP	qq
A; Experiment C; Genetics: A; Genet CES;	1315 EGRIVYGLRPGRSYQPNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRP 1365	ò
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C;Species: C;Date: 15-C	1063 IQILIVSGGLFSKEAQ-TEGRTVPAAVTDLRITENSTRHLSFRWTASEGELSW 1114	È
RESULT 11 T21913 hypothetica	1008 SSYSLIVSWQKAAGVAERYDILLLTENGILLRNTSEPATTKQHKFEDLTPGKKYK 1062	දුරු පු
Db 22:	- :     : :     : :     : :     : :     : :     : :     : :     : :   :   : :   :   : :   :   : :   :   : :   :   : :   :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :   : :	음
.et vo 19	965 BIERGEOVOIMIRSUSGSIKNOIMVOSPTVDAGUOGUIRDNAV 1007	Ş

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 preliminary; translated from GB/EMBL/DDBJ
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: 1-1367 <WIZ>
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 161 HYEVTIKOKONPIQTKSIPKSENECVFVQLVPGRLYSVTVTTKSGQYEANEQGNGRTIPE 820
 321 PVKDLTLRNRSTE-----DLHVTWSGANGD---VDQYEIQL-LFNDMKVPPPFH 865
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 ::: | | | ::|: | | | 3.4 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5 | 1.5
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 321 TDSLITVNW-TPGGGDVDSYITVSAFRHSQKVDSQTIPKHVFEHTFHRLEAGEQYQIMIASV 979
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Caenorhabditis elegans
-Oct-1999 #sequence_revision 15-Oct-1999. #text_change 09-Jul-2004
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preliminary; translated from GB/EMBL/DDBJ
 to the EMBL Data Library, September 1995
e number: 219486
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 to the EMBL Data Library, June 1995
e number: Z19530
n: T22211
 3P:F44G4.8
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--GSNRNTTDSLWFNWSPASGDFDFYELILYNPNGTKKENWKDKDLTEWRFQGLVPGRKY 1238
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A57064
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Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O precursor - human
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C;Species: Homo sapiens (man)
C;Species: 03-Oct-1995 #sequence_revision 08-Peb-1996 #text_change 22-Jun-1999
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Rividgins, K.C.; Wiggins, J.E.; Goyal, M.; Wharram, B.L.; Thomas, P.E.
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	WFNWSPASGDFDFYELILYNPNG  :  WYYNPRV WY-TESRTAPSPPSLMSFADIA  KVTAESRTAPSPPSLMSFADIA  S           SSTISFITAPSPPSLMSFADIA  NKKSEGRIVYGLRPGRSYQFNV	SVTÄCT	SIRRDRPLSVHLMLGQKGNRKTSCPIKINQFEGHF
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8 6 6 6 6 6	8 8 8 8 8 8	8 8 8 8 8 8 8	8 6 8 6 8 6 8 6 8 6

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protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O precursor - rabbit
N.Alternate names: GLEPP1; glomerular epithelial protein 1
N.Contains: protein tyrosine phosphatase phi, cytosolic form; protein tyrosine phosphata
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: A53661
R;Thomas, P.E.; Wharram, B.L.; Goyal, M.; Wiggins, J.E.; Holzman, L.B.; Wiggins, R.C.
A;Thomas, P.E.; Wharram, B.L.; Goyal, M.; Wiggins, J.E.; Holzman, L.B.; Wiggins, R.C.
A;Title: GLEPP1, a renal glomerular epithelial cell (podocyte) membrane protein-tyrosine
A;Reference number: A53661
A;Reference number: A53661
 A/ACCESTORIAL ASSOCIATION AND ACCESTORIAL AND
 1008 SSYSLIVSW--OKAAGVAERYDILLITENGILLRNTSEPATTKO--HKF--EDLTPGKKY 1061
 67;
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 770
 948 KVDSQTIPKHVFEHTFHRLEAGEQYQIMIASVSGSLKNQINVVGRTVPASVQGVIADNAY 1007
 102 GNVVTK------PSR--SITVLTK-------PLPVTSVSIYDY 129
 ::| | | :: ::| | 1330 KPSPETGVLFEIHYPEKYNVFTRVNISYWEGKAFRTMLYKDFFKGKTVFNHW--LPGICY 187
 ---PEHLVNTAT-----SGDV 895
 QOSAFIEGFTVDSAVKNIHI-----SPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQ 947
 | :| : : | : : : | : : : | 288 -SDYETTSQPYWWDSASATPESEDEFVSVLPMEYENNNTLSEAEKPTPAPF-----SF 339
 340 FPVQMILSWLPPKPPTAFDGFHIHIERE----ENFTEYSTVDEEAHEFVAELKEPG-KY 393
 61
 714 TRSGKYENHSFSQER---TVPDKVQGVSVSNSARSDYLRVSWVHATGDFDHYEVTIKNKN
 655 GRNDYLSVSWL-VAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTIT
 771 NFIQTKSIPKSENECVFVQLVPGRLYSVTVTTKSGQYEANEQGNGRTIPEPVKDLTLRNR
 248 PEESFWRS---PETIEKORIFHFTEETPEPSG-----NISSGWPDFNS-----
 Query Match 8.7%; Score 908.5; DB 1; Length 1187; Best Local Similarity 25.0%; Pred. No. 2.4e-42; Matches 366; Conservative 202; Mismatches 474; Indels 423; Gaps
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		EGRIVYGLRPGRSYQFNVKTVSGDSWKTYSKPIFGSVRTKPDKIQNLHCRPQNST 1369	AGMTSEVVEDSTITMIDRPPPPPPHIRVNEKDVLISKSSINFTVNCSWFSDTNGAVKYFT 1489		GKLPYNWSKNGLKCRKLINbVQLDDFDAYIKDMAKDSDYKESLQFEELKLIGLDIPHFAA 928   LLPENRGKNRYNNILPYDATRVKLSNVDDFDAYIKDAYIPGANFREKIJIGLDIPHFAA 928   LLPENRGKNRYNNILPYDATRVKLSNVDDFDAYINASYIPGANFREKIJIGLDFDEGT 1782   LLPENRGKNRYNNILPYDATRVKLSNNBEBGADYINAANYIPGYNSPQEYIATQGPLPET 988   LLPENRCKNRYTNILLPYDFSRVRLLSMNBEBGADYINAANYIPGYNSPQEYIATQGPLPET 988   LLPENRCKNRYTNILLPYDFSRVRLLSMNBEBGADYINAANYIPGTLQMLSESVLPEWT 1842   LLPENRCKNRYTNILLPYDFSRVRCDHYMPPTEEPIAYGDLIYVEMISEEGQDDWA 1048   LLPENRCKNLCGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPT 1900   LLPENRCKGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVRTVRDYINRSPGAGPT 1900   LLPENRCKGEEQLDAHRLIRHFHYTVWPDHGVPETTQSLIQFVHWVRQQATKSKGPM 1103	VVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHMVQTECQYVTLHQCV 1960
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protein-tyrosine-phosphatase (EC 3.1.3.48) U2 precursor - human C;Species: Homo sapiens (man)

RESULT 14

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Cincession: 560613
Ribering, H.; Sawabe, T.; Inazawa, J.; Tsuruo, T.
Oncogne 10, 1731-1738, 1995
A; Tsuruo, T.
Oncogne 10, 1731-1738, 1995
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 1142 UD37 STRHLSFR-----WTASEGELSWYNIFLYNPDG-NLQERAQVDFLVQSFSFQ--- 1142
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 ---KQHKF--EDLTPGKKYKIQILTV--SGGLFSKEAQTEGR----TVPAAVTDLRITEN 1096
 ----NILOGRMYKMVIVTHSGEL---SNESFIFGRTVPASVSHLRGSNRNTTDSLWFN 1193
 .240 LWVVTHSGDLS--NKVTAESRTAPSPPSLMSFADIANTSLAITWKGPPDWTDYNDFE-LQ 1296
 862
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 317 LPMEYENNSTLSETEKSTSGSFSFPPVQMILTWLPPKPPTAFDGFHIHIEREENFTEYLM 376
 434
 609 TWVTWGDPELSCCDSSTISFITAPVAPEITS-VEYFNSLLYISWTYGDDTTDLSHSRMLH 667
 TRSGKYENHSFSQER---TVPDKVQGVSVSNSARSDYLRVSWVHATGDFDHYEVTIKNKN 770
 ---GESKNYFFFFFFFFFNSTLPPPV------IFKASY-HGL----YYIITLVVVN 101
 771 NFIQTKSIPKSENECVFVQLVPGRLYSVTVTTKSGQYEANEQGNGRTIPEPVKDLTLRNR 830
 EIPSGNISSGWPD------FNSSDYETTSQPYWWDSASAAPESEDEFFSV 316
 188 SNITFQLVCEATFNKSTVVEYSGVSHEP-KQHR----------TAPYPPQN 227
 61
27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 228 ISVRIVNLNKN---NWEEQSG---NFPEESFMRSQ----DTIGK---EKLFHFTE--ETP
 492 SKPIIENLVPGAQYQVVIYLRKGPLIGPPSDPVTFA-IVPTGIKDLMLYPLGPT-AVVLS
 GARRILPILWLFVLFKNATAFHVTVQDDNNIVVSL-----EAS-DVISPASVXVVKIT
 : | : : | : : | : : | : : | 435 KPQHVEFHVLSSTTALMSWTSSQEN---YNSTIVSVVSLTCQKQKESQRLEKQYCTQVNS
 550 WTRPYLGVFRKYVVEMFYFNP-ATMTSEWTTYYEIAATVSLTASVRIANLLPAWYYNFRV
 GRNDYLSVSWL-VAPGDVDNYEVTLSHDGKVVQSLVIAKSVRECSFSSLTPGRLYTVTIT
 831 STE-----DLHVT-----WSGANGDV----DQYEIQLLFNDMKVFP---
 ---PFHLV-----NTATEYRFTSLTPGRQYKILVLTISGDVQQSAFIEGFTVPSAVKN
 IHISPNGATDSLTVNWTPGGGDVDSYTVSAFRHSQKVDSQTIPKHVFEHTFHRLEAGEQY
 973 QIMIASVSGSLKNQINVVGRTVPASVQGVIADNAYSSYSLIVSWQKAAGVAERYD----
 WS-PASGDFDFY--ELILYNPNGTKKENW-----KDKDLT-EWRFQGLVPGRKY---V
 Query Match 8.6%; Score 906.5; DB 2; Length 1216; Best Local Similarity 25.0%; Pred. No. 3.2e-42; Matches 377; Conservative 190; Mismatches 459; Indels 484; Gaps
 1028 ILLLTENGILLRNTS---------EPATT---
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Db 599 VYWV	A:Cross-references: GDB:305504  A:Man nnaftion: 19013.4-19013.4
Qy 1239 VLWVVTHSGDLSNKVTABSRTAPSP	
Db 573 LQNETQTKNSVMLWWKAPGD	A; Residues: 1-118 «MATO» A; Residues: 1-118 «MATO» A; Residues: 1-118 «MATO»
Qy 1179 LRGSNRNTTDSLWFNWSPASGDFDF	A;Reference number: A49724; MUID:94124561; PMID:8294459 A;Accession: A49724
516	J. Biol. Chem. 269, 2075-2081, 1994 A,Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase an
Qy 1125 NLQERAQVDPLVQSFSFQNL	C;Accession: A49724 R;Matozaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K
Db 465 RGSRQNVSISTVPNAVTSLSKQDWT	C;Species: Homo Bapiens (man) C;Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
Qy 1073 FSKEAQTEGRTVPAAVTDLRITENS	protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
Db 414 PYPQDYTYWVGYTGDGGGTE	:
Qy 1022VAERYDILLITENGIL	
Db 359 EPGCLYVFSVWVG-KNGINSSR	Db 1205 ISDVIYENVS 1214
Qy 967 EAGEQYQIMIASVSGSLKNQINVV-	QY 1976 PLFPIYENVN 1985
DD 306 TVEAQ-TNSSIALTWEVPDGPDPQN	Db 1148 ALDRILQHIRDHEFVDILGLVSEMRSYRMSMVQTBEQYIFIHQCVQLMWMKKKQQFC 1204
Qy 914 HISPNGATDSLTVNW-TPGGGDVDS	LOOLDSK
	DD 1090 QDVMHFNYTAWPDHGVPTANAAESILQFVHMVRQQATKSKGPMIHCSAGVGRTGTFI 1147
Qy 799 TV-TTKSGQYEANEQGNGRIIPEPV	CY 1798 IVMVTQCVEKGRVKCDHYWPADQDSLYYGDLILQMLSESVLPEWTIREFKIGGEGUDAH 1857
Db 148 QNSTYGVEYTGDGGRAGTRSTAHTN	Db 973 PYDFSRVRLVSMNEEEGADYINANYIPGYNSPQEYIATQGPLPETRNDFWRMJLQQKSQI 1032
Qy 753VHATGDFDHYE	GY 1738 PYDATRUKLSNVDDDPCSDYINASYIPGNNFRREYIVTQGPLPGTKDDFWKMVWEQNVHN 1797
: :   : Db 89 LGPGSLYTCSVWVEKDGVNSSVGTV	Db 913 KLTNPVQLDDFDAYIKDMAKDSDYKFSLQFEELKLIGLDIPHFAADLPLNRCKNRYTNIL 972
Qy 702 LTPGRLYTVII-TTRSGKYENHSFS	OY 1678 KTSCPIKINOFEGHFMKLQADSNYLLSKEYEBLKDVGRNQSCDIALLPBNRCKNRYNNIL 1737
 31 NPGRNLTVETQTTSSISLSWEVPDG	DD 853 RECGAGTFANCASLERDGKLPYNCRRSIFAFLTLLPSCLWTDYPLAFYINPWSKNGLKKR 912
Qy 653 NSGRNDYLSVSWLVAPG	PLSVH
Best Local Similarity 24.0%; Pred. Matches 335; Conservative 154; Mi	799DSPSV-PTFIAVSTMVTEMNPNVVISVLAILSTLLIGLLLVTLIILRKKKHLQMA
F;1028/Binding site: substrate phosphat	Db 772 -AVSPHVVTIS 798
F.1022/Active Bite: CyB (phosphocystein	Qy 1533 CAENPNSNSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLFDEDL 1592
F;762-7/8/Domain: transmembrane #Status F;779-1118/Domain: intracellular #Status	Db 739 VTLLWVEEGVADFFKVFFQHVGSSQKTKLQBPV771
bronectin type bronectin type	QY 1473 VNCSWPSDTNGAVKYPTVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQTNYFASK 1532
bronectin	Db 719 VKLS 738
bronectin type	Qy 1413 MMLVPHKRYLVSIKVQSAGMTSEVVEDSTITMIDRPPPPPPPHIRVNEKDVLISKSSINFT 1472
bronectin type	Db 706CTERGSNT
F;28-110/Domain: ilbronectin type III r	OY 1353 TKPDKIQNLHCRPQNSTAIACSWIPPDSDFDGYSIECRKMDTQEVEFSRKLEKEKSLLNI 1412
C; Keywords: carcinogenesis; duplication F;1-27/Domain: signal sequence #status	Db 668 WMVVTEGKKKIKKSVTRNVMTAILSLPPGDTYNLSVTT705
A; Note: highly expressed in colon and p C; Superfauily: protein-tyrosine-phospha	OY 1297 WLPRDALTVENPYNNRKSEGRIVYGLRPGRSYOFNVKTVSGDSWKTYSKPIFGSVR 1352

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and pancreatic cancer cells but not in the normal cell:
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turn; glycoprotein; phosphoprotein; phosphoric monoes
III repeat homology <3FNA>
--phosphatase, receptor type H #status predicted <MAT>
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e 6	135/ KIQNEHCKFÜNSTAIACSWIFPDSDFDGTSIECKKMDTQEVEFSKKLEKEKSLLNIMMLV 1416  VASSTQSLCASTYPD
o o o	1417 PHKRYLVSIKVQSAGMTSEVVEDSTITMIDRPPPPPPPPPPRINVNEKDVLISKSSINFTVNCS 1476
දු යු	1477 WFSDTNGAVKYFTVVVREADGSDELKPEQQHPLPSYLEYRHNASIRVYQTNYFASKCAEN 1536 
දු පු	1537 PNSNSKSFNIKLGAEMESLGGKRDPTQQKFCDGPLKPHTAYRISIRAFTQLF 1588 
දු පු	1589 DEDLKEFTKPLYSDTFFSLPITTESEPLF-GAIEGVSAGLFLIGMLVAVVALLICRQKVS 1647 138 D-GMKVVSHSVVCHTESAGVIAGAFVGILLFLILVGLIFFLKRRNK 783
& a	1648 HGRERPSARLSIRRDRPLSVHLNLGQKGNRKTSCPIKINQFEGHFWKLQADSNYLLSKEY 1707 184 KKQQKPELRDLVFSSPGDIPAEDFADHVRKNERDSNCGFADEY 826
& 43	1708 EELKDVGRNQSCDIALLPENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNN 1767 
è 8	1768 FRREYIVTOGPLPGTKDDFWKMVNEONVHNIVMVTQCVEKGRVKCDHYWPADQDSLYYGD 1827 
oy Bb	1828 LILOMLSESVLPEWTIREFKICG-EEQLDAHRLIRHFHYTVWPDHGVPETTQSLIOFVRT 1886     : : :     :
Oy Db	1887 VRDYINRSPGAGFTVVHCSAGVGRTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRVHM 1946 
<b>&amp;</b> 43	1947 VQTECQYVYLHQCV 1960                1065 VQTEAQYVPLHQCI 1078

Search completed: March 10, 2006, 18:37:54 Job time : 63.7073 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
 Copyright
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March 10, 2006, 18:19:33 ; Search time 193.96 Seconds (without alignments) 4932.432 Million cell updates/sec protein search, using sw model OM protein -. 0 Run

7095 1 MESKVLLAVALWLCVETRAA......GSTAQILQPDSGTTLSSPPV 1356 US-10-633-742-6 Perfect score: Sequence: **Title:** 

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Bult Query No. Score Match Length DB I 1 7092 99.9 1356 1 V

	script	P35968 homo sapien	Q59eb0 homo sapien		008775 rattus norv	Q8vcd0 mus musculu	P35918 mus musculu	Q677ml gallus gall	P52583 coturnix co	Q5git4 brachydanio		_	Q5git2 brachydanio	Q5md89 brachydanio	P35917 mus musculu	Q5su94 mus musculu	Q91zt1 rattus norv	P35916 homo sapien	. P17948 h vascular	Q5tarl homo sapien	homo	homo s	gallı		Q4sjq3 tetraodon n	P35969 mus musculu	Q8axb3 brachydanio	Q5git3 brachydanio	Q4jdd5 brachydanio	Q5tz34 brachydanio	) rattuB	O5duf3 gallus gall
	ID	VGFR2 HUMAN	OSSEBO HUMAN	QSPQUO_RAT	VGFR2 RAT	Q8VCD0 MOUSE	VGFR2 MOUSE	Q677M1 CHICK	VGFR2 COTJA	Q5GIT4 BRARE	Q4RKW3 TETNG	P79701_COTCO	Q5GIT2_BRARE	Q5MD89 BRARE	VGFR3 MOUSE	Q5SU94 MOUSE	Q91ZT1_RAT	VGFR3 HUMAN	VGFR1 HUMAN	QSTARI_HUMAN	Q86W07_HUMAN	Q86W08 HUMAN	Q8QHL3_CHICK	VGFR1_RAT	04SJQ3 TETNG	VGFR1 MOUSE	VGFR2 BRARE	Q5GIT3 BRARE	Q4JDD5_BRARE	QSTZ34_BRARE	Q91ZTO RAT	OSDUF3 CHICK
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p ,	Query	99.66	99.9	87.2	9.98	86.5	86.0	71.8	70.9	46.0	43.1	42.0	40.3	40.2	39.5	٠	39.3		38.7	38.7	38.6	38.5	37.7	•	37.1	37.0	36.3	•	33.5	٠	31.9	31.0
	Score	7092	7091	6183.5	6143.5	6135.5	6100.5	5091	5031.5	3264.5	3058.5	2981.5	2858.5	2855.5	2804	2804	2790	2751.5	2748.5	2746.5	2742	2734.5	2677	2648	2631	2623.5	2573.5	2387	2376	2275.5	2264.5	2196.5
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32 34 44	35	9 7 4 9 6 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4444.

## ALIGNMENTS

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P35968 060723; Old 178: 014178; Old 178: 01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
(VEGRR-2) (Kinase insert domain receptor) (Protein-tyrosine kinase receptor Flk-1).
Name=KDR; Synonyms=FLK1;
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
 Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D., Armellino D.C., Gospodarowicz D., Boehlen P.; Identification of the KDR tyrosine kinase as a receptor for vascular endothelial cell growth factor...; Biochem. Biophys. Res. Commun. 187:1579-1586 (1992).

-!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein kinase activity. The VEGF-kinase ligand/receptor signaling system
 NUCLEOTIDE SEQUENCE OF 1-22.
MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;
Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.,
 "Cloning and functional analysis of the promoter for KDR/flk-1, a receptor for vascular endothelial growth factor."; J. Biol. Chem. 270:23111-23118(1995).
 TISSUE-Umbilical vein;
MEDLINE=92019839; PubMed=1656371;
Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.,
 "Identification of a new endothelial cell growth factor receptor
 Yin L.Y., Wu Y., Patterson C.;
"Full length human KDR/flk-1 sequence.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
 TISSUE-Umbilical vein;
Yu Y., Whitney R.G., Sato J.D.;
"Coding region for human VEGF receptor KDR (VEGFR-2).";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
1356 AA.
 MEDLINE=93038639; PubMed=1417831;
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 tyrosine kinase.";
Oncogene 6:1677-1683(1991).
 Homo sapiens (Human)
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 Harber E.;
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 Shows
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 (Potential).
(Potential).
(Potential).
(Potential).
 (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
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0
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Pred. No. 0;
1; Mismatches 0; Indels 0
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0 -> H (in dbSNP:1870377).

/FTId=VAR 02053.

0 -> E (in Ref. 2).

A -> T (in Ref. 3).

R -> G (in Ref. 3).

R -> N (in Ref. 3).

V -> E (in Ref. 3).

V -> E (in Ref. 3).
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 (in dbSNP:2305948)
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Best Local Similarity 99.9
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 DR HGNC, HANGLESON,

DR HGNC, HANGLESON,

DR GO, GO:0005897. C:integral to plasma membrane; TAS.

GO; GO:0005201; F:vascular endothelial growth factor receptor. .; TAS.

DR GO; GO:00005021; F:vascular endothelial growth factor receptor. .; TAS.

DR GO; GO:0000169; P:transmembrane receptor protein tyrosine kin. .; TAS.

DR InterPro; IPR003194; PGC kinase.

DR InterPro; IPR003246; Tyr_pkinase.

DR InterPro; IPR003246; Tyr_pkinase.

DR InterPro; IPR003144; VEGFR.

DR InterPro; IPR003144; VEGFR.

DR RINTS; PR018314; VEGFRECEPTOR.

DR RINTS; PR01834; VEGFRECEPTOR.

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DR RINTS; PR01834; VEGFRECEPTOR.

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DR PROSTITE; PS03040; IG LIKE; 5.

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DR PROSTITE; PS00109; PROTEIN KINASE TOW; 1.

DR PROSTITE; PS00109; PROTEIN KINASE TOW; 1.

DR PROSTITE; PS00109; PROTEIN KINASE TOW; 1.

DR PROSTITE; PS00109; PROTEIN KINASE TOW; 1.

DR PROSTITE; PS00109; PROTEIN KINASE TOW; 1.

DR PROSTITE; PS00109; PROTEIN KINASE TOW; 1.

RW Notlectide binding; Phosphorylation; Polymorphism; Rinase.

KW Nucleotide binding; Phosphorylation; Polymorphism; Rinase.

FT CHAIN 20 1356 Veneror I Transmembrane; Tyrosine-protein kinase.

FT CHAIN 20 1356 Veneror I Transmembrane; Tyrosine-protein kinase.

FT CHAIN 20 1356 Veneror I Transmembrane; Tyrosine-protein kinase.

FT CHAIN 20 1356 Veneror I Transmembrane; Tyrosine-protein kinase.

FT CHAIN 20 1356 Veneror I Transmembrane; Tyrosine-protein kinase.

FT CHAIN 20 1356 Veneror I Transmembrane; Tyrosine-protein kinase.

FT CHAIN 20 1356 Veneror I Transmembrane; Tyrosine-protein kinase.

FT CHAIN 20 1356 Veneror I Transmembrane; Tyrosine-protein kinase.
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plays a key role in vascular development and regulation of vascular permeability.

CATALYIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBLILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF receptor subfamily.

SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
 autocatalysis) (By
 (Potential). (Potential). (Potential).
 Extracellular (Potential) Potential.
 Cytoplasmic (Potential).

19-11ke C2-type 1.

19-11ke C2-type 2.

19-11ke C2-type 3.

19-11ke C2-type 5.

19-11ke C2-type 6.

19-11ke C2-type 6.

19-11ke C2-type 7.

Pyotean kinase.

ATP (By similarity).

By similarity).

Phosphotyrosine (by autoc similarity).

Phosphotyrosine (by autoc similarity).

Phosphotyrosine (by autoc similarity).

Phosphotyrosine (by autoc similarity).

Phosphotyrosine (by autoc similarity).

Phosphotyrosine (by autoc similarity).

Phosphotyrosine (by autoc similarity).

Phosphotyrosine (by autoc similarity).

Phosphotyrosine (by autoc similarity).
 EMBL; AF035121; AAB88005.1; -; mENA.
EMBL; AF063658; AAC16450.1; -; mENA.
EMBL; KG1656; CAA43837.1; -; mENA.
EMBL; L04947; AAA59459.1; -; mENA.
EMBL; X89776; CAA61916.1; -; Genomic_DNA.
 PIR; JC1402; JC1402.
PDB; 1VK2; X-ray; A=806-1171.
Ensembl; ENSG0000128052; Homo sapiens.
HGNC; HGNC:6307; KDR.
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96
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66
96
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TOPO DOM
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9 9 120

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 Yokoyama
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 SEBABLIKLIBIGVQTGSTAQILQPDSGTTLSSPPV 1356
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RRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020
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 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFROGKDYVGAIPVDLK 1055
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 LOITCRGORDLD
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161601
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 Gaps
 GO:0005524; F:ATP binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO:0005021; F:vascular endothelial growth factor receptor. .
GO:0006468; P:protein amino acid phosphorylation; IEA.
GO:0007169; P:transmembrane receptor protein tyrosine kin.
 13;
 Length
 Indels
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PROSITE; PSS0011; PROTEIN KINASE DOW; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS001040; RECEPTOR TYR KIN III; 1.
SEQUENCE 1343 AA; 150274 WW; F4B906E8012ASC59 CRC64;
 DB 2;
 98;
 87.2%; Score 6183.5;
86.3%; Pred. No. 0;
tive 75; Mismatches
GO, GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonin
GO; GO:0005021; F:vascular endothelial gr
GO; GO:0005021; F:vascular endothelial gr
GO; GO:0007169; P:transmembrane receptor
InterPro; IRR001359; IQ.
InterPro; IRR00110; Ig-1ike.
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InterPro; IRR001245; Tyr_pkinase.
InterPro; IRR00134; VEGFR.
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Best Local Similarity 86.3
Matches 1170; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 TISSUE=Lung;
Director MGC Project;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO87029; AAH87029.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
 Created)
Last sequence update)
Last annotation update)
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 SEEAELLKLIEIGVOTGSTAOILOPDSGTTLSSPPV 1451
 Sci. U.S.A. 99:16899-16903(2002)
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 OSPQUO RAT PRELIMINARY;
OSPQUO;
O1-FEB-2005 (TrEMBLrel. 29, C:
O1-FEB-2005 (TrEMBLrel. 29, L:
Kdr protein.
 Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
 NUCLEOTIDE SEQUENCE.
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 CMEEEEVCDPKFHYDNTAGISHYLQNSKRKSRPVSVKTFEDIPLEEFEVKVIPDDSQTDS
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 GRGAFGQVIEADAFGIDKTATCKTVAVKALKEGATHSEHRALMSELKILIHIGHHLAVVN
 SRKCIHRDLAARNI LLSEKNVVKI CDFGLARDI YKDPDYVRKGDARLPLKWMAPETI FDR
 DCWHGEPSQRPTPSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 DCWHEDPNQRPAFSELVEHLGNLLQANAQOGKDYIVLPMSETLSMEEDSGLSLPTSPVS
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
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 VYTIQSDVWSFGVLLWEI FSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 |:|| |||||:::
SDEAGLLKLVDVAGHV-----DSGTTLRSSPV 1343
 1257
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RESULT 4
VGFR2 RAT

ID VGFR2 RAT

LO 008775;

AC 008775;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 48, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)

DE VBGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase DE 1).

Name=Kdr; Synonyms=Flkl;

OS Rattus norvegicus (Rat).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;;

OC Bukaryota; Muriade; Murinae; Rattus.

OC Muroidae; Murinae; Rattus.

OX NNEL_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Retina;
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MCD: 9955; Kdr.

RGD; G0:0019838; F:growth factor binding; IMP.

RGD; G0:0019838; F:growth factor binding; IMP.

RGD; G0:0019818; F:growth factor binding; IMP.

RGD; G0:0048010; P:vascular endothelial growth factor receptor. .; IMP.

RGD; G0:0048010; P:vascular endothelial growth factor receptor. .; IMP.

InterPro; IPR001359; Ig.C2.

RINTERPRO; IPR00134; RECEPTOR,
 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
 system
 kinase family. CSF-1/PDGF
 (By
 + a protein
Wen Y., Edelman J.L., De Vries G.W., Sachs G.;
Submitted (WAR-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
kinase activity. The VEGF-kinase ligand/receptor signaling sy
plays a key role in vascular development and regulation of
vascular permeability (By similarity).
--- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a proteit
tyrosine phosphate.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- SUBCELLULAR LOCATION: Type I membrane from thinase family. CSF-1/P
 (Potential).
 receptor subfamily.
SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
 autocatalysis)
 (Potential)
 Vascular endothelial grown
receptor 2.
Extracellular (Potential)
 Potential.
Cytoplasmic (Potential).
Ig-like C2-type 1.
Ig-like C2-type 2.
Ig-like C2-type 4.
Ig-like C2-type 5.
Ig-like C2-type 5.
Ig-like C2-type 5.
Ig-like C2-type 7.
Protein kinase.
ATP (By similarity).
 By similarity.
ATP (By similarity).
Phosphotyrosine (by a similarity).
N-linked (GlcNAc. . . .
 (GlcNAc.
(GlcNAc.
(GlcNAc.
 N-linked
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N-linked
 EMBL; U93306; AAB97508.1; -; mRNA.
EMBL; U93307; AAB97509.1; -; mRNA.
HSSP; P35968; 1VR2.
 749
1158
844
1024
864
 46
96
143
158
 46
96
143
158
 domains
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TRANSMEM
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1020 1016 1080 1076 1140

926

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STRAIN=FUB/N; TISSUE=Kidney;

WEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

A Itschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.M.; Schuler G.D.;

A Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.R.; Bhat N.K.;

A Diatchenko L.; Marusia K.F.; Farmer A.A.; Rubin G.M.; Hong L.;

A Diatchenko L.; Marusia K.F.; Farmer A.A.; Rubin G.M.; Hong L.;

B Diatchenko L.; Marusia K.F.; Casavant T.L.; Scheetz T.E.;

B Rownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

R Raha S.S.; Loquellano N.A.; Peters G.J.; Abramanon R.D.; Mullahy S.J.;

B Dosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gibbs R.A.;

R Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

A Hilalon D.K.; Muzny D.W.; Sodergren E.J.; Lu X.; Gibbs R.A.;

B Antillalon D.K.; Muzny D.W.; Scherman M.; Madrigues S.; Sanchez A.;

R Halt S. M.; Touchman J.W.; Green E.D.; Dickson M.C.;

R Radriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

B Butterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

B Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
 1137 DCWHEDPNQRPAFSELVEHLGNLLQANAQQDGKDYIVLPWSETLSMEEDSGLSLPTSPVS
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 837 GRGAFGOVIEADAFGIDKTATCKTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 RRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 CMEEBEVCDPKFHYDNTAGISHYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDSQTDS
 GMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
 SRKCHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWAAPETIFDR
 1017 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDPRLPLKWMAPETIFDR
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 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 Last sequence update)
 1321 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 |:|| |||||::
SDEAGLLKLVDVAGHV-----DSGTTLRSSPV
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 PRT; 1345
 Kinase insert domain protein receptor.
Name=Kdr;
 Created)
 QBVCDO MOUSE PRELIMINARY;
QBVCDO;
01-MAR-2002 (TYEMBLFEL: 20,
01-MAR-2002 (TYEMBLFEL: 26,
01-MAR-2004 (TYEMBLFEL: 26,
 Mus musculus (Mouse).
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NUCLEOTIDE SEQUENCE
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 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
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 EIKWYKNGI PLESNHTI KAGHVLTIMEVSERDTGNYTVILTNPI SKEKOSHVVSLVVYVP
 POIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
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 Gaps
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 13;
 86.6%; Score 6143.5; DB 1; Length 1343;
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 80; Mismatches 102; Indels
 CRC64;
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 MW; AD7E509EB62D3FF4
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 (GlcNAc.
 Pred. No. 0;
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 150394
 85.6%;
 Best Local Similarity 85.6
Matches 1161; Conservative
 245
318
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LKRRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEF 1018
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 01-07N-1994 (Rel. 29, Created)
01-07N-1994 (Rel. 29, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
(VBGTR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase
 937 PLGRGAFGQVIEADAFGIDKTATCKTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNV
 597 LTPVCKNLDALWKLNGTWFSNSTNDILIVAFQNASLQDQGDYVCSAQDKKTKKRHCLVKQ
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 MLDCWHEDPNQRPSFSELVEHLGNLLQANAQQDGKDYIVLPMSETLSMEEDSGLSLPTSP
 YSSEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
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 (Kinase NYK).
 Name=Kdr; Synonyms=Flk-1, Flk1;

 STANDARD;
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 WDSKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSV 238
 GEKLVLNCTARTELINVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVT 298
 RSDOGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYP 358
 PPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKOSHVVSLVVY 418
 VPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEECCANEPSQAVSVTN 478
 476
 9
 9
Generation and initial analysis of more than 15,000 full-length human
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 WLWPINIQSGSEQRVEVTEC--SDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYV
 QDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRIS
 Gaps
 15;
 Length 1345;
 GO; GO: 000565; C: extracellular space; TAS.
GO; GO: 000565; C: extracellular space; TAS.
GO; GO: 004546; P: cell fate commitment; IMP.
GO; GO: 004544; P: cell migration; IGI.
GO; GO: 004546; P: endothelial cell differentiation; IDA.
InterPro; IPR007110; Ig-like.
InterPro; IPR001834; RecepttyrkinsIII.
InterPro; IPR001834; RecepttyrkinsIII.
InterPro; IPR001845; Tyr_pkinase.
InterPro; IPR001845; Tyr_pkinase.
InterPro; IPR009134; VEGFR.
InterPro; IPR009134; VEGFR.
InterPro; IPR009134; VEGFR.
InterPro; IPR009134; VEGFR.
 Query Match 86.5%; Score 6135.5; DB 2; Length Best Local Similarity 85.9%; Pred. No. 0; Matches 1166; Conservative 71; Mismatches 106; Indels
 Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020530; AAH20530.1; -; mRNA.
HSSP; 35966; 1VR2.
Ensembl; ENSWUSGO000062960; Mus musculus.
MGI; MGI:96683; Kdr.
 1345 AA; 150460 MW; 11859F8A58A33A39 CRC64;
 PRINTS; PRO1832; VEGERECEPTOR.
PRINTS; PRO1832; VEGERECEPTR2.
PRODOM; PRO1001; PROC. Kina8e; 2.
SMART; SM00409; Proc. Kina8e; 2.
SMART; SM00409; TyrKc; 1.
PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS500107; PROTEIN KINASE DOM; 1.
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PROSITE; PS00109; PROTEIN KINASE DOM; 1.
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Kidney;
Director MGC Project;
 Kinase, Receptor
SEQUENCE 1345
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PRINTS; PRO1832; VEGFRECEPTOR.

PRINTS; PRO1834; VEGFRECEPTOR.

PRO1834; VEGFRECEPTOR.

PRO1834; VEGFRECEPTOR.

PRO1834; VEGFRECEPTOR.

SMART; SM00408; IGC2; I.

SMART; SM0019; TYKC; I.

SMART; SM0019; TYKC; I.

PROSITE; PS50011; PROTBIN KINASE ATP; I.

PROSITE; PS50010; PROTBIN KINASE TYR; I.

PROSITE; PS00109; PROTBIN KINASE TYR; I.

RAGIOGENESIS; ATP-binding; Developmental protein; Differentiation;

Magiogenesis; ATP-binding; Developmental protein; Differentiation;

Mycoprotein; Immunoglobulin domain; Kinase; Nucleoride-binding;

Mycoprotein; Receptor; Repeat; Signal; Transmembrane;

Tyrosine-protein kinase.

Potential.
 P -> T (in Ref. 1).
G -> D (in Ref. 3).
L -> VI (in Ref. 1).
S -> C (in Ref. 1).
GUTSCLNGSGPVPAPPTPGNHERGAA -> RSPPV (in
 Phosphotyrosine (by autocatalysis) (By
 Potential.
Vascular endothelial growth factor
 GO:0005615; C:extracellular space; TAS.
GO:0045165; P:cell fate commitment; IMP.
GO:0016477; P:cell migration; IGI.
GO:0045446; P:endothelial cell differentiation; IDA.
GO:003097; P:hemopoiesis; IMP.
GO:001570; P:vasculogenesis; IMP.
 Cytoplasmic (Potential).
19-11ke C2-type 1.
19-11ke C2-type 2.
19-11ke C2-type 3.
19-11ke C2-type 5.
19-11ke C2-type 5.
19-11ke C2-type 6.
19-11ke C2-type 7.
Protein kinase.
ATP (By similarity).
By similarity.
ATP (By similarity).
 Extracellular (Potential)
Potential.
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 Ensembl; ENSMUSG0000062960; Mus musculus.
MGI; MGI:96683; Kdr.
 InterPro; IPR007110; Ig-1ike.
InterPro; IPR001398; Ig c2.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR001824; ReceptryrkinsIII.
InterPro; IPR001845; Tyr_pkinase.
InterPro; IPR001345; Tyr_pkinase_AS.
InterPro; IPR009134; VEGFR.
InterPro; IPR009134; VEGFR.
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 STRAIN=BALB/c; TISSUE=Embryo;
MEDLINES9220880; PubMed=7681362; DOI=10.1016/0092-8674(93)90573-9;
Millauer B., Wisigmann-Voos S., Schnurch H., Martinez R.,
Mueller N.P.H., Risau W., Ullrich A.;
High affinity VEGF binding and developmental expression suggest Flk-1
as a major regulator of vasculogenesis and angiogenesis.";
Cell 72:835-846(1993).
 MEDLINE-93141255; PubMed-8423989; Ochizicha R.D., Raid H.T., Bernard O., Ziemiecki A., Wilks A.P.; MCHYK/FLK-1: a putative receptor protein tyrosine kinase isolated from ElO embryonic neuroepithelium is expressed in endothelial calls of the
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
Muroidea; Muridae; Murinae; Mus.
 MEDLINE=93361481; PubMed=8356051;

Quinn T.P., Peters K.G., de Vries C., Ferrara N., Williams L.T.;

Quinn T.P., Reters K.G., de Vries C., Ferrara N., Williams L.T.;

Quinn T.P., Ranse I is a receptor for vascular endothelial growth
factor and is selectively expressed in vascular endothelium.";

Proc. Natl. Acad. Sci. U.S.A. 90:7533-7537(1993).

-I. FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein

kinase activity. The VEGF-kinase ligand/receptor signaling system
plays a key role in vascular development and regulation of
vascular permeability.

-I. CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed at high levels in adult heart, lung, kidney, barain and skeletal muscle, but is also expressed at lower levels in most other adult tissues.
SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
 "A receptor tyrosine kinase cDNA isolated from a population of enriched primitive hematopoietic cells and exhibiting close genetic linkage to c-kit."; Proc. Natl. Acad. Sci. U.S.A. 88:9026-9030(1991).
 "Cloning and functional analysis of the promoter for KDR/flk-1, a receptor for vascular endothelial growth factor."; J. Biol. Chem. 270:23111-23118(1995).
 Patterson C., Perrella M.A., Hsieh C.-M., Yoshizumi M., Lee M.-E.
 receptor subfamily.
SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
 NUCLEOTIDE SEQUENCE.
STRALN=C3H/He; TISSUB=Fetal liver;
MEDLINE=92020984; PubMed=1717995;
Mathews W., Jordan C.T., Gavin M., Jenkins N.A., Copeland N.G.,
Lemishcka I.R.;
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MEDLINE=96032749; PubMed=7559454; DOI=10.1074/jbc.270.39.23111;
 EMBL; X70842; CAA50192.1; -; mRNA.
EMBL; X59397; CAA42040.1; -; mRNA.
EMBL; S53103; AAB25043.1; -; mRNA.
EMBL; X89777; CAA61917.1; -; Genomic_DNA.
PIR; A41228; A41228.
 Oncogene 8:11-18(1993).
 tyrosine phosphate.
musculus (Mouse)
 NUCLEOTIDE SEQUENCE.
 NUCLEOTIDE SEQUENCE
 developing embryo."
 NCBI_TaxID=10090;
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Harber E.;

FUNCTION

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domains.

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(Potential)

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ProDom; PD000001; Prot_kinase;
SMART; SM00409; IG; 7.
SMART; SM00408; IGc2; 5.
 PRINTS; PR01832; VEGFRECEPTOR
PRINTS; PR01834; VEGFRECEPTR2
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 NUCLEOTIDE SEQUENCE.
 NCBI_TaxID=9031;
 Hashimoto T.;
 Name=Flk1;
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 LKRRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEF 1018
 WDSKKGFTIPSYMISYAGMVPCEAKINDESYQSIMYIVVVOGYRIYDVVLSPSHGIELSV 238
 361 APDIKWYRNGRPIESNYTMINGDELTIMEVTERDAGNYTVILTNPISMEKQSHMYSLVVN 420
 658
 WLWPNNQSGSEQRVEVTEC -- SDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYV 118
 QDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRIS 178
 GEKLVLACTARTELAVGIDFAWEYPSSKHQHKKLVARDLKTQSGSEMKKFLSTLTIDGVT 298
 PPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVY 418
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 PYPCEEWRSVEDFQGGNKIEVNKNOFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGR 538
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 9
 1 MESKALLAVALWFCVETRAASVGLPGDFLHPPKLSTQKDILTILANTTLQITCRGQRDLD
 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
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Ref. 3).
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 1367 AA;
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EMBL; AY382882; AAR26285.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:actin binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004671; F:receptor activity; IEA.
GO; GO:0005021; F:vascular endothelial growth factor receptor.
GO; GO:0005021; F:vascular endothelial growth factor receptor.
GO; GO:0005021; F:vascular endothelial growth factor receptor.
GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. 11 CHICK
0677M1 CHICK PRELIMINARY; PRT; 1348 AA.
0677M1,
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Vascular endothelial growth factor receptor 2. |||:|| ||||::: | | || || || ||::: | | || || || || ||::: | YSSERAELLKLIEIGVQTGSTAQILQPDSGTTL 1351 InterPro; IRR001899; Actbind_actnin.
InterPro; IRR001899; Ig.
InterPro; IRR001899; Ig.
InterPro; IRR001899; Ig.
InterPro; IRR001898; Ig.c2.
InterPro; IRR001849; ReceptryrkinsIII.
InterPro; IRR001849; ReceptryrkinsIII.
InterPro; IRR001849; Receptryrkinse.
InterPro; IRR001849; Fort pkinase.
InterPro; IRR001849; Igr pkinase.
InterPro; IRR001849; Igr pkinase.
InterPro; IRR001849; VEGFR.
InterPro; IRR009184; VEGFR.

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1131 IMLDCWHGDPKQRPTFSELVEHLGNLLQANVRQDGKDYVVLPLSVSLNMEEDSGLSLPTS
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 LKRRLDSITSSQSSASSGFVEEKSLSDVEEEEA-PEDLYKDFLTLEHLICYSFQVAKGME
 FLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKMMAPETI
 1011 FLASRKCIHRDLAARNILLSDNNVVKICDFGLARDIYKDPDYVRKGDARLPLKWAAPETI
 FDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQ
 1071 FDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQ
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 PVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQ
 TDSGMVLASEELKTLEDRTK-LSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDT
 1250 TDSGMVLASEELKTLEERDKQVKIPFSTLAPSKSNESVMSEASNQTSGYQSGYHSDDMDT
 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
(Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
(VBGFR-2) (Endothelial kinase receptor EK1) (Quek 1) (Quek1).
Name=KDR; Synonyms=EK1, FLK-1;
Coturnix coturnix japonica (Jananase quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Flamme I., Breier G., Risau W.; "Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-are expressed during vasculogenesis and vascular differentiation in
 TISSUE=Spinal cord,
MEDLINE=93378866; PubWed=8396413; DOI=10.1016/0925-4773(93)90096-G;
Bichmann A., Marcelle C., Breant C., Le Douarin N.M.;
"Two molecules related to the VEGF receptor are expressed in early endothelial cells duting avian embryonic development.";
Mech. Dev. 42:33-48(1993).
 MEDLINE=95301109; PubMed=7781909; DOI=10.1006/dbio.1995.1180;
 1317 TVYSSEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 1310 MVCSSEDTELLCAQEAS-PTLPRVHGLVHDSPAPLVSPPL 1348
 NUCLEOTIDE SEQUENCE OF 764-880, AND CHARACTERIZATION
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 NUCLEOTIDE SEQUENCE OF 910-1348.
 STANDARD;
 NCBI_TaxID=93934;
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 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD
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 RVISFHVTRGPEITLOPDMOPTEQESVSLWCTADRSTFENLTWYKLGPOPLPIHVGELPT
 PVCKNLDTLWKLNATMF-SNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQL
 TVLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGN
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 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
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 EIKWYKNGI PLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPI SKEKQSHVVSLVVYVP
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 Gaps
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 SMART; SM00219; TYTKC; 1.

PROSITE; PS00019; ACTININ 1; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; RECEPTOR IN KINASE DOM; 1.
 Receptor.
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 61
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 118
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 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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 the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
 prays a new total in vascular development and regulation or vascular permeability.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFFCITY: In all endothelial tissues during onset of vascularization. In later development, present in lung, heart, intestine and skin.
-!- DBVELOPMENTAL STAGE: Expressed in whole mesoderm at onset of gastrulation. From day 2, confined to endothelial tissues and expression continues to be widespread throughout vascularization until E9 where it becomes treatricted to specific regions such as the spinal chord and heart valves.
-!- INDUCTION: In vitro, it is induced by basic fibroblast growth factor (bFGF), uniquely in the first 24 hours of cell culture.
-!- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF
 [4]
NUCLECTIDE SEQUENCE OF 1023-1079.
PubMed=1281306;
Marcelle C., Eichmann A.;
"Molecular cloning of a family of protein kinase genes expressed in the avian embryo.";
 the avian embryo.";
Oncogene 7:2479-2487(1992).
-!- FUNCTION: Receptor for VEGF or VEGFC. Has a tyrosine-protein
kinase activity. The VEGF-kinase ligand/receptor signaling syste
plays a key role in vascular development and regulation of
 SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
 Vascular endothelial growth factor
 Extracellular (Potential)
 Cytoplasmic (Potential) .
Ig-like C2-type 1.
Ig-like C2-type 2.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig c2.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR001824; ReceptryrkinsIII.
InterPro; IPR001845; Tyr_pkinase.
InterPro; IPR0098466; Tyr_pkinase_AS.
InterPro; IPR009134; VEGFR.
InterPro; IPR009134; VEGFR2.
 receptor 2
 EMBL, X83288; CAA58268.1; -; mRNA.
EMBL; S65205; AAB28127.1; -; mRNA.
EMBL; S78345; AAB34594.1; -; mRNA.
PIR, JC4953; S51656:
quail embryo.";
Biol. 169:699-712(1995)
 P35968; 1VR2
 21
757
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43
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70.9%; Score 5031.5; DB 1; Length 1348;
Best Local Similarity 72.1%; Pred. No. 7.7e-289;
Matches 960; Conservative 144; Mismatches 212; Indels 15;
 (Potential)
 (Potential)
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MW; A5E4194A76FD5FB3 CRC64;
Ig-like C2-type 3.
Ig-like C2-type 4.
Ig-like C2-type 5.
Ig-like C2-type 6.
Ig-like C2-type 7.
Protein kinase.
ATP (By similarity).
ATP (By similarity).
 N-linked (GlcNAc. N-linked (GlcNAc.
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144 KTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFCEAK 203
 266 ----HEKRSVNGSMSTSRYKTSSNKRKLMNSLELSNTLTVENVTLNDTGEYICTASSGQM 321
 430 SPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAV--SVTNPYPCEEWRS 487
 149 --VVIPCLVSVEDLAVTLYTKYPVKELSTDGKEVIWDSRRGFILPSRVVSYAGVVYCQTT
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 30 DPPILNITEKTIKINASDTLQITCRGRQILEWSTPHNRTSSETKLTISDCSGDGLFCSTL
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 315 TKKNSTFVRVHEKPFVAFGSGMESLVEATVGE-RVRIPAKYLGYPPPEIKWYKNG--IPL
 372 ESNHTIK--AGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVPPQIGEKSLI
 30 DLPRLSIQKDILTIKANTTLQITCRGQRDLDWLWPNNQSGSEQRVEVTECS-DGLFCKTL
 204 INDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYP
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 DB 2;
 Match 46.0%; Score 3264.5; DB 2;
Local Similarity 50.3%; Pred. No. 3.7e-184;
es 678; Conservative 195; Mismatches 370;
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 10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
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10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Receptor tyrosine kinase Kdr.
Name=kdrb; Synonyms=kdr;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
 NUCLEOTIDE SEQUENCE.
Habeck H., Langhoff J., Vogel A.M., Trowe T., Koblizek T.I.,
 PRT; 1357 AA
 QSGIT4 BRARE PRELIMINARY;
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VAFGSGMESLVEATVGERV-RIPAKYLGYPPPEIKWYKNGIPLESNHIIKAG-HVLTIME 387
 6 SLELTCSGRQYLHWITPRISS----RFSIGDCSGSGLFCTILRISNATVNETGQYQCSYK 61
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens B.,
Dasilya C., Salanoubat M., Levy M., Boudet N., Castellano S.,
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Craud C., Lardier S., Brottier P., Coutanceau J.P., Gouzy J.,
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Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander W., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
The early vertebrate proto-karyotype.";
Lindure 431:946-957(2004).
 48 TLQITCRGQRDLDWLWPNNQSGSEQRVEVTECS-DGLFCKTLTIPKVIGNDTGAYKCFYR
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ORFNames-GSTENG00032761001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
 which
 Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.

EMBL, CAAEO1015025; CAG10969.1; -; Genomic_DNA.

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5.7e-172;
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 Match 43.1%; Score 3058.5; Local Similarity 47.0%; Pred. No. 5.7e-ies 638; Conservative 203; Mismatches
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 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL 780
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(TrEMBLrel. 31, Last sequence update)
(TrEMBLrel. 31, Last annotation update)
SCAF15025, whole genome shotgun sequence.
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Q4RKW3, TETNG PRELIMINARY;
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 954 AIPVDLKRRLDSITSSQSSASSGFVEEKSLSDVBEEEAPEDLYKDFLTLEHLICYSFQVA 1013
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-WAX-2004 (TrEWBLrel. 26, Last annotation update)
Vascular endothelial growth factor receptor.
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P79701_COTCO
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AC P79701_
D7 01-MAY-1997 (TrEMBLrel. 03,
D7 01-MAR-2004 (TrEMBLrel. 03,
D7 01-MAR-2004 (TrEMBLrel. 26,
D8 Vascular endothelial growth
G8 Name-Quek2,
G8 Name-Quek2,
G9 Coturnix coturnix (Common que
CC Eukaryota; Metazoa; Chordata
OC Archosuuria; Aves; Neognatha
OC Coturnix.
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Coturnix coturnix (Common quail). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,

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 162
 281 QMQRAVIESERRSLQTHTELS---SILTLHNVSQQDLGRYTCTAINGAQMLEESTDVIVH 337
 EKPFVAFGSGMESLVEATVG-ERVRIPAKYLGYPPPEIKWYKNG--IPLESNHTIKAGHV 382
 66
 9
 28
 221 NKVFKSNPFIIHIAGIELYDIQLYPKKAMELLVGEKLVLNCTVWAEFNSGVRFQWTYPGK
 61 WLWP-----NNQ-----SGSEQRVEVTECSDGLFCKTLTIPKVIGNDTG
 100 AYKCFYRETD-----LASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVI----
 117 YYHCYYKYIDAKIEGTTAVSAYIFVRDFEQPFI------NKPETLLISKKEN
 149 ---PCLGSISNLNVSLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFCEAKIN
 DESYQSIMYIVVVGYRIYDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSS
 266 KHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVH
 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
MEDLINE=97017121; PubMed=8863722; DOI=10.1016/0378-1119(96)00159-X; Eichmann A., Marcelle C., Breant C., Le Douarin N.M.; "Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor (VEGF) receptor-like molecules.";
 R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0015224; F:ATP binding; IEA.

R GO; GO:0005524; F:Receptor activity; IEA.

R GO; GO:0005021; F:vascular endothelial growth factor receptor. . .;

R GO; GO:0005021; F:vascular endothelial growth factor receptor. . .;

R GO; GO:0005021; F:vascular endothelial growth factor receptor. . .;

R GO; GO:0005021; F:vascular endothelial growth factor receptor. . .;

R O: GO:0005021; F:vascular endothelial growth factor receptor. . .;

R InterPro; IPR00116; Ig-11ke.

R InterPro; IPR00119; Prot Kinase.

R InterPro; IPR0011824; RecepttyrkinsIII.

R InterPro; IPR001245; Tyr_Dkinase.

R InterPro; IPR00134; VGGFR.

R InterPro; IPR00137; VGGFR.

R InterPro; IPR00137; VGGFR.

R InterPro; IPR00137; VGGFR.
 Length 1379;
 101;
 Indels
 1379 AA; 156962 MW; 8411621AEF565520 CRC64;
 Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
 PRINTS; PRO1832; VEGFRECEPTOR.
PRINTS; PRO1835; VEGFRECEPTR3.
PRODOM; PRO10015; Prot kinase; 2.
SMART; SM00408; IGC2; 3.
SMART; SM00408; IGC2; 3.
SMART; PRO195; PYKC; 1.
PROSITE; PS50815; IG LIKE; 5.
PROSITE; PS50011; PROTEIN KINASE ATP; UNKNOWN_1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
 42.0%; Score 2981.5; DB 2; 46.0%; Pred. No. 2.2e-167;
 Best Local Similarity 46.0%; Pred. No. 2.2e-167;
Matches 639; Conservative 208; Mismatches 440;
 EMBL; X83287; CAA58267.1; -; mRNA
HSSP; P35968; 1VR2.
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Habeck н., Langnori
Schulte-Merker S.;
 PROSITE; PS50011;
PROSITE; PS00109;
PROSITE; PS00240;
 Cyprinidae, Dani
NCBI_TaxID=7955;
 Kinase, Recepto
 Name=flt4;
 SEQUENCE
 Query Match
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 966 ITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMFFLASRKCI 1025
 SDVWSFGVLLWEIPSLGASPYPGVQINEEFCQRFXDGTRWRAPEYTTAEIYRIMLSCWHG 1166
 HRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQ 1085
 SDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHG 1145
 EPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVSCMERE 1205
 DSGMVLASEBLKTLEDRTKLSPSFGGMVPSKSRBSVASEGSNQTSGYQSGYHSDDTDTTV 1318
 |||||||||| : :|:| : | : | DSGMVLASEEFERIENRHRKEGGFSSKGPNRTAE-LSAEQSDLRGRCRPSYGSQVGGQTF 1341
 DF-DMRIRCHSLAARYYNCVSFPGCLTGGNQIRCSSRIKTFEEFPMTHTMYKAHP-DNQT 1282
 511 AVNPIESIDTWVEFVEGRNKTVSKLAIQEANVSAMYKCIASNKVGRDERLIYFYVTTIPD 570
 GPEIESQPSEEPIEGQDLQLSCNADNYTYENLQWYRLANLSKLHDEEGNPLVLDCKNVHHY 630
 --IKDVAEHHAGTYTLVLRNRLVGLEKRISLQLIVNVPPRIHEKETSSP--SIYSRRSPQA 450
 451 LICIVYGIPAPEVIQWQWRPWMPCRMFSRRSLNSRHRAARRHQRDRMPECKDWKDVSRQD 510
 --EITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPTPVCKNL-DT 608
 RTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPLGRGAFG 846
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 KPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFR-QGKDYVGAIPVDLKRRLDS 965
 ------PCEEWRSVEDFQ 492
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 VRKEDEGLYTCOACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWLLLVIIL 786
 QVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACT 906
EKPPINVEWRKGPVIEATAGDEAVKLPVKVVAYPQPDFQWYKAGKLIPKQSQSSMQ----
 GGNKIEVNKNOFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGP-
 PTITGNLENOTTSIGESIEVSCTASGNPPPQIMMPKDNETLVEDSGIVLKDGNRNLTIRR
 EVCDPKF-----HYDNTAGISQYLQNSKRKSRPVSVKTPEDIPLEEPEVKVIPDDNQT
 LTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQT
 LTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY---
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YNSEYGEL 1349
 YSSEEAEL 1326
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165 PEKRFVPDGNRISMDSKKGFTIPSYMI----SYAGMVFCEAKINDESYQSIMYIVVVGY 221 IEA. .; IEA DRQGQQSPIDIPGYREIRLKEC-QGVAGKPYCKILILINAQANDSGYYRCFYKDIKAVID 13 IGIPFFSGLVNGFSMSPPTLDNTKDQLVINANDTLNITCRGQRILDWSWPEESLSKVEFT ---NNQSGSE----QRVEVTECSDGL----FCKTLTIPKVIGNDTGAYKCFYRET-----DLASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSL--CARY Brachydanio rerio (Zebrafish) (Danio rerio). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. GO:0015020; C:membrane; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO:0004674; F:receptor activity; IEA.
GO:0005021; F:vescular endothelial growth factor receptor.
GO:0006468; P:protein amino acid phosphorylation; IEA.
GO:000169; P:transmembrane receptor protein tyrosine kin. Ouery Match 40.3%; Score 2858.5; DB 2; Length 1357; Best Local Similarity 45.0%; Pred. No. 4.1e-160; Matches 624; Conservative 221; Mismatches 415; Indels 127; 22 VGLP----SVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLDWLWP--"Synergistic signaling of vegf receptors is required for 1357 AA; 153149 MW; 1A4007911B8CF179 CRC64; vasculogenesis in zebrafish."; Submitred (JAN-2004) to the EMBL/GenBank/DDBJ databases EMBL; AYE24001; AAS92272.1; -; mRNA. ZFIN; ZDB-GENE-990526-326; flt4. Koblizek Last sequence update) Last annotation update) NUCLEOTIDE SEQUENCE. Habeck H., Langhoff J., Vogel A.M., Trowe T., Pfam; PF00047; ig; 5.
Pfam; PF00047; ig; 5.
Pfam; PF00047; ig; 5.
PRINTS; PR01832; VEGFRECEPTOR.
PRINTS; PR01835; VEGFRECEPTOR.
ProDom; PD000001; Prot. Kinase; 2.
SWART; SW00409; IG; 6.
SWART; SW00219; TC; 1.
SWART; SW00219; TYC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1. RECEPTOR TYR KIN III; 1 InterPro; IRR003599; Ig.
InterPro; IRR00110; Ig-like.
InterPro; IRR00110; Ig-like.
InterPro; IRR000119; Prot kinase.
InterPro; IRR001824; RecepttyrkinsIII.
InterPro; IRR001845; Tyr pkinase.
InterPro; IRR001845; Tyr pkinase.
InterPro; IRR009184; Tyr pkinase.
InterPro; IRR009184; Tyr pkinase.
InterPro; IRR009134; VEGFR3. 10-MAY-2005 (TrEMBLrel. 30, Cre 110-MAY-2005 (TrEMBLrel. 30, Las 10-MAY-2005 (TrEMBLrel. 30, Las Receptor tyrosine kinase Flta. 166 셤 ò

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RESULT 12 QSGIT2_BRARE

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---NOTSG---YOSGY-HSDDTDTTVY
 65 ---NNOSGSE----QRVEVTECSDGL----FCKTLTIPKVIGNDTGAYKCFYRET----
 13 IGIPFFSGLVNGFSMSPPTLDNTKDQLVINANDTLNITCRGQRILDWSWPEESLSKVEFT
 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
 Gaps
 GO:0016524; F:ATP binding; IEA.
GO:0004674; F:ATP binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO:0005021; F:vascular endothelial growth factor receptor. .
GO:0006468; P:protein amino acid phosphorylation; IEA.
GO:0007169; P:transmembrane receptor protein tyrosine kin. .
 127;
 Length 1357;
 22 VGLP-----SVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLDWLWP-
 Indels
 SMART; SM00409; IG; 6.
SMART; SM00409; IG; 6.
SMART; SM00209; STKC; 1.
SMART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN KINASE APP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
SEQUENCE 1357 AA; 153177 WW; D68C197828BE278E CRC64;
 databases.
 Last sequence update)
Last annotation update)
 2;
 Match 40.2%; Score 2855.5; DB 2; Local Similarity 44.9%; Pred. No. 6.2e-160; es 623; Conservative 222; Mismatches 415;
 Lawson N., Moore J.;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ
EBBL; AY833404; AAV93318.1; -; mRNA.
ZFIN; ZDB-GENE-980526-326; flt4.
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 1357
 InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR003110; Ig-11ke.
InterPro; IPR000119; Prot kinase.
InterPro; IPR001824; RecepttyrkinsIII.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR008266; Tyr pkinase.
InterPro; IPR009134; VEGFR:
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 Created)
 --LSPSFGGMVPSK--SRESVASEGS
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 01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29, 01-FEB-2005 (TrEMBLrel. 29, Flt4.
 QŠMD89_BRARE PRELIMINARY;
QSMD89;
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 --SSEEA 1324
 NUCLEOTIDE SEQUENCE.
 1350 FSSSDQA
 Name=flt4;
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 SDVEEEEAP-EDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVV 1042
 .000 STINPPRVTVDDLWKTPLIIEDLICYSFQVARGMEFLASRKCIHRDLAARNILLSENNVV 1059
 KICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLHWEIFSLG 1102
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 LLQENSLPE-----IPFNVSQSSEDDGFSQASSRPPSQEEIRLACNTLPTRYYNCVPFA 1233
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 340
 509
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 424
 TVILTN-PISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHH 455
 482
 541
 999
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 IEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVL 743
 803
 IVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCR 863
 601
 LSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLKRRLDSITSSQSSASGFVEEKSL 983
 TVAVKOLKEGATASEHKALMSELKILIHIGNHLNVVNLLGACTKPNGPLMVIVEYCKYGN
 EATVGER-VRIPAKYLGYPPPEIKWYKNGIPLESNHTIK---AGHVLTIMEVSERDTGNY
 IHWYWQLEEECANEPSQAV----SVTNPYPCEEWRSVEDFQGGNKIEVNKNQFALIEG
 KNKTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMQPTEQES
 VSLWCTADRSTFENLTWYKLGPQPLPIHVGELPTPVCKNLD---TLWKLNATMFSNSTND
 ILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLTVLERVAPTITGNLENQTTSIGES
 TVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGN
 RIYDVVLSPSHG-IELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQ
 SGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLV
 GCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLS
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
GISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDSGMVLASEELKTLEDRTK- 1277
 Vortice Standard, PRT; 1363 AA.
Vortice Standard, PRT; 1363 AA.
P35917;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Vascular endothehial growth factor receptor 3 precursor (EC 2.7.1.112)
VacRR-3) (Tyrosine-protein kinase receptor FLT4).
Name=Flt4; Synonyms=Flt-4;
 GCVMVGPSSTCHSR----VKTFEELPMEMTSHKT-QHDSQTDSGMVLASDELERFEHKHRG
 --LSPSFGGMVPSK--SRESVASEGS-----NQTSG---YQSGY-HSDDTDTTVY
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Mammalia, Eutheria, Euarchoncoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
 tyrosine phosphate.
--- SUBCELLUAR LOCATION: Type I membrane protein.
--- TISSUB SPECIFICITY: Expressed in adult lung and liver, and in fetal liver, brain, intestine and placenta.
--- SIMILARITY: Belongs to the Tyr protein kinase family. CSF-1/PDGF receptor subfamily.
--- SIMILARITY: Contains 7 Ig-like C2-type (immunoglobulin-like)
 MEDLINE-93330572; PubMed-8393164; Innerty H., Kelleher K., Morris G.E., Bean K., Merberg D.M., Kriz Morris J.C., Sookdeo H., Turner K.J., Mood C.R.; Molecular cloning of murine PLT and PLT4.";
 activity.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 "Chromosomal localization of FLT4, a novel receptor-type tyrosine
 Genomics 13:475-478(1992).
-!- FUNCTION: Receptor for VEGFC. Has a tyrosine-protein kinase
 Galland F., Karamysheva A., Mattei M.-G., Rosnet O., Marchetto
 HSSP; P35968; 1VR2.
Ensembl; ENSMUSGO0000020357; Mus musculus.
MG1; MG1:95561; Flt4.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005515; F:protein binding; IPI.
 EMBL; L07296; AAA40077.1; -; mRNA.
PIR; IS8375; IS8375.
 NUCLEOTIDE SEQUENCE OF 1033-1072.
 Oncogene 8:2293-2298(1993)
 --SSEEA 1324
 1350 FSSSDQA 1356
 Mus musculus (Mouse)
 [1]
NUCLEOTIDE SEQUENCE.
 NCBI_TaxID=10090;
 STRAIN=C57BL/6J;
 PubMed=1319394;
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 1163 LLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVSCMEEEEVCD--PKFHYDNT--A 1218
 1120 ASPYPGIQIDEDFCKRLKDGTRMRAPDNASPEIYGIMLACWQGEPRERPTFPALVEILGD 1179
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 509
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 SGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLV 340
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 TVILIN-PISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHH 455
 683
 -DLASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSL--CARY 165
 222 RIYDVVLSPSHG-IELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQ 280
 VSLWCTADRSTFENLTWYKLGPQPLPIHVGELPTPVCKNLD----TLWKLNATMFSNSTND 623
 IEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVL 743
 GCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLS 803
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 IHWYWQLEEECANEPSQAV----SVTNPYPCEEWRSVEDFQGGNKIEVNKNQFALIEG
 PEKRFVPDGNRISWDSKKGFTIPSYMI----SYAGMVFCEAKINDESYOSIMYIVVVGY
 EATVGER-VRIPAKYLGYPPPEIKWYKNGIPLESNHTIK----AGHVLTIMEVSERDTGNY
 ILIMBLKNASLQDQGDYVCLAQDRKTKKRHCVVRQLTVLERVAPTITGNLENQTTSIGES
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 ----ETDLASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLC 162
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 KARIEGTTAASTYVEVRDEKHPFINKPDT-----LLVNRKDSMWVPCLVSIPGLNITL-
 -RSQSSALHPDGQEVLMDDRRGMRVPTQLLRDALYLQCETTWGDQNFLSNLFVVHITGNE
 :|:
TELS---SILTIHNVSQNDLGPYVCEANNGIQRFRESTEVIVHEKPFISVEWLKGPVLEA
 TVG-ERVRIPAKYLGYPPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILT
 VKWLKEGATASEHRALMSELKILIHIGNHLNVVNLLGACTKPNGPLMVIVEFCKYGNLSN
 ARYPEKRFVPDGNR1SWDSKKGFT1PSYM1SYAGMVFCEAKINDESYQSIMY1VVVVGYR
 IYDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSG
 SEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEA
 NPI SKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQ
 LEBEC----ANEPSQAVSVTNPYP-CEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTL
 462 PWTPCKTFAQRSLRRRQQRDGMPQCRDWKEVTTQDAVNPIESLDSWTEFVEGKNKTVSKL
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 MELKNASLODGGDYVCLAQDRKTKKRHCVVRQLTVLERVAPTITGNLENQTTSIGESIEV
 SCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCOACSVLGCA
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 818 DPGEVPLEEQCEYLSYDASQWEFPRERLHIGRVLGHGAFGKVVBASAFGINKGSSCDTVA
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 927 YLRSKRNEFVPYKTKG----ARFRQGKDYVGAIPVDLKRRLDSITSSQSSASSGFVEEKS
 938 FLRVKRDTFNPYAEKSPEQRRRFRA---MVEGAKADRRRP----GSSDRALFTRFLMGKG
 LSDVEEEEAP----EDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLS
 ---SARRAPLVQEAEDLWLSPLTWEDLVCYSFQVARGWEFLASRKCIHRDLAARNILLS
 EKNVVKI CDFGLARDIYKDPDYVRKGDARLPLKMMAPETIFDRVYTIQSDVWSFGVLLWE
 1098 IPSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELV
 DPDELPLDEHCERLPYDASKWEFPRDRLKLGKPLGRGAFGQVI EADAFGIDKTATCRTVA
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 MESKVLLAVALWLCVETRAASVGLPS-VSLDLPRLSIQKDILTIKANTTLQITCRGQRDL
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R PRIMES, PR008137; VEGER.

R PRIMES, PR018135; VEGERECEPTOR.

R PRIMES; PR018135; VEGERECEPTR3.

R PRONONO1; Prot kinase; 2.

R SMRAT; SM00408; IGG2; 2.

R SMRAT; SM00149; TYKC; 1.

R PROSITE; PS50013; PROTEIN KINASE ATP; 1.

R PROSITE; PS00101; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE TYP; 1.

R PROSITE; PS00101; PROTEIN KINASE TYP; 1.

R PROSITE; PS00101; PROTEIN KINASE TYP; 1.

R PROSITE; PS00101; PROFEIN TYR KIN III; 1.

M ATP-binding; Glycoprotein; Immunos Jobulin domain; Kinase; Nucleotide-binding; Phosphorylation; Receptor; Repeat; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
 (Potential)
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 k; Score 2804; DB 1; Length 1363;k; Pred. No. 7e-157;207; Mismatches 465; Indels 102;
 Vascular endothelial growth receptor 3.
 Potential.
MW; FlBF8A2BDEF99BE9 CRC64;
 Extracellular (Potential)
 Cytoplasmic (Potential)
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TP (By similarity).
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Ig-like C2-type 1.
Ig-like C2-type 3.
Ig-like C2-type 4.
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Ig-like C2-type 6.
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Protein kinase.
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 InterPro, IPR003598; Ig_c2.
InterPro, IPR00719; Prot kinase.
InterPro, IPR001824; RecepttyrkinsIII.
InterPro, IPR001245; Tyr_pkinase.
InterPro, IPR008266; Tyr_pkinase_AS.
InterPro, IPR009134; VEGFR.
 Potential
 N-linked
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Ig-like.
 39.5%;
 153016
 Query Match
Best Local Similarity 44.1<sup>§</sup>
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 SLAARYYNCVSFPGRLARGTKTPGSSRMKTFRELPM-TPTTYKASMDNQTDSGMVLASEB 1283
 LKTLEDRIKLSPSFGGWVPSKSRESVASEGSNQ-----TSGYQSGYHSDDTDTTVYSSE 1322
 1284 FEELESRHRPEGSFSCKGPGQHMDIPRGHPDPQGRRRRRPTQGAQGG-----KVFYNNE 1336
 PWTPCKTFAQRSLRRRQQRDGMPQCRDWKEVTTQDAVNPIESLDSWTEFVEGKNKTVSKL 521
 SCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCA
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 VM/LKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLST
 YLRSKRNEFVPYKTKG----ARFRQGKDYVGAI PVDLKRRLDSITSSQSSASSGFVEEKS
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 MELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLTVLERVAPTITGNLENQTTSIGESIEV
 LSDVEEEEAP----EDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLS
 IFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELV
 VIQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMQPTEQESVSLWCTAD
 RSTFENLTWYKLGPQPLPIHVGELPTPVCKNLDTLWKLNATMFSNSTND-----ILI
 EHLGNILLOANA-QODGKDYIVLPISETLSMEEDSGLSLPTSPVSCME-EEEVCDPKFH--
 NSAAGLRQNISLELVVNVPPHIHEKEASSP-SIYSRHSRQTLTCTAYGVPQPLSVQWHWR
 LEEEC---ANEPSQAVSVTNPYP-CEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTL
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 Search completed: March
Job time : 200.96 secs
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 1284 FEELESRHRPEGSFSCKGPGQHMDIPRGHPDPQGRRRRPTQGAQGG-----KVFYNNE 1336
 11.7 KARIEGTTAASTYVFVRDFKHPPINKPDT-----LLVNRKDSWWVPCLVSIPGLNITL- 169
 TAGDELVKLPVKLAAYPPPEFQWYKDRKAVTGRHN---PHALVLKEVTEASAGVYTLALM 402
 NPISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQ 461
 ----ETDLASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLC 162
 ARYPEKRFVPDGNRISWDSKKGPTIPSYMISYAGMVPCBAKINDESYQSIMYIVVVVGYR 222
 -RSQSSALHPDGQEVLWDDRRGMRVPTQLLRDALYLQCETTWGDQNFLSNLFVVHITGNE 228
 SEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEA 342
 DWLWPNNQ-----SGSEQRVEVTECSDGL----FCKTLTIPKVIGNDTGAYKCFYR-- 106
 IYDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSG 282
 TVG-ERVRIPAKYLGYPPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILT 401
 57
 <u>..</u>
 EHIGNILIGANA-QODGKDYIVLPISETISMEDSGLSLPTSPVSCME-EREVCDPKFH--
 ----YDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDSGMVLASEE
 Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
 MESKVLLAVALWICVETRAASVGLPS-VSLDLPRISIOKDILTIKANTTLOITCRGORDL
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 Query Match 39.5%; Score 2804; DB 2; Length 1363; Best Local Similarity 44.1%; Pred. No. 7e-157; Matches 610; Conservative 207; Mismatches 465; Indels 102;
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 SEQUENCE 1363 AA; 153015 MW; FIBF8A2BDEF99BE9 CRC64;
 Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases EMBL; AL646088; CAI25911.1; -; Genomic_DNA.
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FMS-like tyrosine kinase 4.
Name=Flt4; ORFNames=RP23-58E13.1-001;
 PRT;
 Q5SU94_MOUSE PRELIMINARY;
 (FEB-2005)
 Mus musculus (Mouse)
 NUCLEOTIDE SEQUENCE
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 EAEL 1326
 NCBI_TaxID=10090;
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March 10, 2006, 18:19:09; Search time 146.073 Seconds (without alignments) 4078.762 Million cell updates/sec

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Perfect score:

1 MESKVLLAVALWLCVETRAA.......GSTAQILQPDSGTTLSSPPV 1356 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

2443163 Total number of hits satisfying chosen parameters:

2443163 segs, 439378781 residues

Searched:

length: 0 length: 200000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:* geneseqp1980s:* Genesed Database

geneseqp2003bs:* geneseqp2004s:* geneseqp2003as:* geneseqp2000s:4 geneseqp2002s:* geneseqp2001s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

## SUMMARIES

Description	Aay97783 Human KDR	Human	Aay97576 Human Flk	Abr40196 Human vas	Human	Human	Human	Adh17130 Human vas	Adq39806 Human myo	Human	Adr46648 Cancer-as	Adt92353 Human vas	Adv90285 Protease-		Adz26561 Human VEG	Aau79426 Human Kin	Adg70543 Human KDR	Abu64302 Human KDR	Aaw80997 Human rec	Aau79427 Human Kin	Human	Aau79429 Human Kin	Aar26999 Novel typ	Aaw59275 Human KDR
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ID	AAY97783	AAB62475	AAY97576	ABR40196	ADD08954	ABM79007	ADF45097	ADH17130	ADQ39806	ADQ39808	ADR46648	ADT92353	ADV90285	ADY59385	AD226561	AAU79426	ADG70543	ABU64302	AAW80997	AAU79427	AAU79430	AAU79429	AAR26999	AAW59275
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& Query Match	100.0	99.9	99.9	99.9	99.9	6.66	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	99.9	6.66	99.9	99.9	9.66	99.6
Score	7095	7092	7092	7092	7092	7092	7092	7092	7092	7092	7092	7092	7092	7092	7092	7091	7091	7090	7087	7087	7087	7087	7070	7070
Result No.	-	7	8	4	S	9	7	60	0	10	11	12	13	14	15	16	17	18	19	20	21		23	24

Adz00446 VEGFR-2.	Adq39807 Human myo	Adr32338 Rat optim	Adr32351 Rat recep	Abm79009 Murine Fl	Abr40197 Murine va	Aar31377 Human £1k	Aar37504 Murine fl	Aar44996 Murine fl	Aar67537 Mouse flk	Aar97420 Murine fo	Aaw19875 Murine fl	Adp90725 Mouse foe	Aay08618 Murine fl	Abg70917 Mouse rec	Aae25820 Murine re	Adw87791 Murine fe	Aeb46056 Murine fl	Aar28041 flk-1. 3/	Aar67817 Flk1 rece	Aar54046 Sequence
ADZ00446	ADQ39807	ADR32338	ADR32351	ABM79009	ABR40197	AAR31377	AAR37504	AAR44996	AAR67537	AAR97420	AAW19875	ADP90725	AAY08618	ABG70917	AAE25820	ADW87791	AEB46056	AAR28041	AAR67817	AAR54046
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99.5	95.9	87.2	96.6	86.4	86.1	85.9	85.9	85.9	85.9	85.9	85.9	85.9	85.9	85.9	85.9	85.9	85.9	85.9	85.9	85.5
7060	9089	6183.5	6143.5	6127.5	6106.5	6097.5	6097.5	6097.5	6097.5	6097.5	6097.5	6097.5	6097.5	6097.5	6097.5	6097.5	6097.5	6094.5	6091.5	6066.5
25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAY97783 standard; protein; 1356 AA. AAY97783; RESULT 1 AAY97783 

(first entry) 22-AUG-2001

Human KDR/Flk-1 protein.

vasculār endothelial growth factor receptor; VEGF receptor; inflammation; postiasis; rheumatoid arthritis; haemandjoms; leiomyoma; angiofibroma; diabetic retinopathy; endometriosis; macular degeneration; cancer; dimerisation inhibitor; therapy; KDR/FIk-1; human. Immunoglobulin-like domain; Ig-like domain; retinal neovascularisation;

Homo sapiens.

WO200142284-A2.

14-JUN-2001.

07-DEC-2000; 2000WO-GB004693

99GB-00028950. 07-DEC-1999; (METR-) METRIS THERAPEUTICS LID.

Pappa H;

WPI; 2001-381631/40.

growth plays a Novel proteins that prevent dimerization of vascular endothelial factor receptors and for treating diseases in which the receptor role e.g. inflammation, cancer, diabetic retinopathy, psoriasis.

Claim 11; Fig 3; 83pp; English.

retinopathy, angiofibromas, endometriosis, macular degeneration, retinal This sequence represents the human KDR/Flk-1 protein. The invention relates to a protein comprising the amino acid sequence of the fourth immunoglobulin (Ig)-like domain of a vascular endothelial growth factor (VEGF) receptor or a variant of the protein that retains the ability to bind to a VEGF receptor. The protein, its functional equivalent and DNA encoding it are useful for treating a disorder whose parhology is dependent upon a VEGF family-mediated pathway, including inflammation, psoriasis, rheumatoid arthritis, haemangiomas, leiomyomas, diabetic

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 Receptor protein, vascular endothelial growth factor receptor-2; VEGFR-2; neuropilin-1; NP-1; co-receptor; human; angiogenic.
 Determining compounds which bind to a complex comprising vascular endothelial growth factor receptor-2 and Neuroplin-1 to provide superior pro- and anti-angiogenic agents.
 The invention relates to determining whether a compound is capable of binding to a receptor protein complex comprising a vascular endothelial
 SRKCIHRDLAARNILLSBKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWAAPETIFDR
 DCWHGEPSQRPTFSELVEHLEGNLLQANAQOGKDYIVLPISETLSMEEDSGLSLPTSPVS
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 Location/Qualifiers
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/note= "extracellul
124. .320
/note= "Ig domain"
 Claim 7; Page 32-39; 82pp; English.
 protein; 1356
 Human VEGFR-2 receptor protein.
 26-OCT-2000; 2000WO-US029579.
 99US-0162367P
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 (first entry)
 (PROC) PROCTER & GAMBLE
 Rosenbaum JS, Whitaker
 WPI; 2001-308686/32.
N-PSDB; AAF83308.
 AAB62475 standard;
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 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLMVVN 900
neovascularisation or cancer. The protein or its functional equivalents are also useful for inhibiting the dimerisation of a VEGF receptor
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQXDLLTIKANTTLOITCRGQRDLD
 KLVLNCTARTELAVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 WLWPNNQSGSEQRVEVTECSDGLFCKTLT1PKV1GNDTGAYKCFYRETDLASV1YVYVQD
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 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 DOGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 DQGLYTCAASSGLMTKROSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEECANEPSQAVSVTNPY
 RVISFHVIRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 VLERVAPTITGNLENQTISIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKGGATHSEHRALMSELKILIHIGHHLNVVN
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 RVISPHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
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 DB 4; Length 1356;
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ive 0; Mismatches
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Matches 1356; Conservative
 Sequence 1356 AA;
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 (NP-1) receptor protein. One method comprises introducing a sample comprising the compound to the receptor protein and allowing the compound to bind to the complex. Signaling through VEGRR-2 is enhanced in the presence of the NP-1 co-receptor an enhods of the invention can be used for identifying novel pro- and anti-angiogenic compounds. The present sequence represents the human VEGFR-2 receptor protein
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 #INTERPRINGSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 120
 180
 YRSPPIASVSDQHGVVYITENKNKTVVIPCLGSISNINVSLCARYPEKRFVPDGNRISWD 180
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 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN 900
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 KLVLNCTARTELNVGIDFNWEYPSSKHOHKKLVNRDLKTOSGSEMKKFLSTLTIDGVTRS
 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEECANEPSQAVSVTNPY
 PCEEWRSVEDFOGGINKI EVNIKNOPALI EGKNKTVSTLVI QAANVSALYKCEAVNKVGRGE
 RVISFHVTRGPBITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 RVISFHVTRGPEITLOPDMOPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 PVCKNLDTLWKLNATWFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKGRHCVVRQLT
 VLERVAPTITGNLENQTISIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 KLVLNCTARTELNVGIDFNWEYPSSKHOHKKLVNRDLKTOSGSEMKKFLSTLTIDGVTRS
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 PCEEWRSVEDFQGGNKI EVNKNQFALI EGKNKTVSTLVI QAANVSALYKCEAVNKVGRGE
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 VLERVAPTITGNLENQTISIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 Gaps.
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 Length 1356;
 protein and a
 0; Indels
 DB 4;
 Score 7092; DE Pred. No. 0; 1; Mismatches
 (VEGFR-2)
 Query Match
Best Local Similarity 99.9%;
Matches 1355; Conservative
 receptor-2
 Sequence 1356 AA;
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 New nucleic acid encoding angiogenic proteins, useful e.g. for promoting healing of wounds and treating peripheral arterial disease, critical limb ischemia or coronary disease.
 of
 Human; angiogenic protein; wound healing; vascular tissue repair;
peripheral arterial disease; critical limb ischaemia; coronary disease;
angiogenesis; tumour; inflammation; diabetic retinopathy; psoriasis;
rheumatoid arthritis; autoimmune disease; allergy; cancer; therapy;
infectious disease; neurodegeneration; Flk-1.
 in the isolation
 DCWHGEPSORPTFSELVEHLGNLLOANAQODGKDYIVLPISETLSMEEDSGLSLPTSPVS
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 RRLDSITSSOSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPRTIFDR
 DCWHGEPSORPTFSELVEHLGNLLQANAQODGKDY1VLPISETLSMEEDSGLSLPTSPVS
 GWYLASEELKTLEDRIKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
 SRKCIHRDIAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 sequence is a human Flk-1 fragment, and was used
 transmembrane and extracellular domains.
 SEEAELLKLIEIGVOTGSTAQILQPDSGTTLSSPPV
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV
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 standard; protein; 1356
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 99US-0137796P
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 (first entry)
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 Rosen CA, Ruben SM,
 WPI; 2001-071057/08
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 WO200075163-A1
 03-JUN-1999;
 Example 48;
 Human Flk-1
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an angiogenic protein of the invention. The angiogenic proteins and the disease and to detect diseases, or susceptibility, by detecting mutations or the presence or amount of angiogenic protein expression. Particularly they are used to stimulate wound healing, growth of damaged bone and tissue, especially peripheral arterial disease, ratical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat disease, critical limb ischaemia or coronary disease. Antagonists of the sequences are used to inhibit angiogenesis in tumours and to treat cinflammation (where associated with increased vascular permeability), diabetic retinopathy, rheumatoid arthritis or psociasis. Agonists are also used to identify specific binding agents (potential therapeutic agents) and to raise antibodies. The antibodies are useful as therapeutic and to raise antibodies. The antibodies are useful as therapeutic of ant vavo or in viro diagnosis (including imaging) or for therapy (including when linked to e.g. a label or cytcoxin); and for immunotyping of cells, e.g. for detecting minimal residual disease or haematopoietic progenitor/stem cells. It is also contemplated that the sequences might be useful for treating a very ander ange of other diseases, alleryy; and certical, fungal or parasitic); neurodegeneration, also as contemplated that increased to the certical, fungal or parasitic); neurodegeneration, also as contemplated that increased to the certical and the certical and parasitic); neurodegeneration, also as sequence the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and the certical and certical and certical and certical and certical and certical and certical and certical and certical and certical and certical and certical and certical and certical and certical and certical an

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Best Local Similarity 99.9
Matches 1355; Conservative 61 121 61 121 181 181 241 241 301 301 361 361 421 421 481 481 541 541 601

1140 1140 1020 1080 1080 1020 1260 1320 1200 900 780 840 900 960 780 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL GRGAFGQVIEADAFGIDKTATCRTVAVXMLKEGATHSEHRALMSELKILIHIGHHLNVVN GRGAFGQVIEADAFGIDKTATCRTVAVKWLKEGATHSEHRALMSELKILIHIGHHLNVVN 961 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA SRKCIHEDLAARNILLSEKAVVKI CDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR 1081 VYIIQSDVWSFGVLLMEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR 661 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR NITIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL LLVIILRTVRRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEPPRDRLKLGKPL LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK RRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS 1141 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSWEEDSGLSLPTSPVS CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS GMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTTVYS SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR Human; vascular endothelial growth factor receptor-2; cytostatic; angiogenic; antiardingiogenic; antiarthritic; antirheumatic; antisense; VEGFR-2; hyperproliferative disorder; cancer; rheumatoid arthritis; Human vascular endothelial growth factor receptor-2. SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356 \$ ABR40196 standard; protein; 1356 26-SEP-2002; 2002WO-US030734 (first entry) sapiens. angiogenesis 01-AUG-2003 10-APR-2003 721 781 841 1021 1021 1081 1141 1201 1261 1321 199 721 781 841 901 961 1201 ABR40196; Ношо ABR40196 RESULT g 8 셤 à 요 8 셤 8 셤 8 셤 ð 셤 ઠે g δ 셤 셤 원 8 8 ò

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GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHINVVN 900
 RRLDSITSSOSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 LLVI ILRTVKRANGGELKTGYLSI VMDPDELPLDEHCERLPYDASKWEFPRDRLKKGKPL
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 RRLDS1TSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 DCWHGEPSQRPTFSELVEHLGNLLQANAQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 1141 DCWHGEPSQRPTFSELVEHLGNLLQANAQOGKDYIVLPISETLSMEEDSGLSLPTSPVS
 1201 CMEEEEVCOPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIILVGTAVIAMFFWL
 1LV1 I LRTVKRANGGELKTGYLS I VMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
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 VYTIQSDVWSFGVLLWEI FSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 GWLLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
PVCKNLDTLWKLNATMFSNSTNDILIMBLKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 nervous system function; cancer; ischaemia; cerebral infarction;
cerebral bleeding; Alzheimer's disease; myocardial infarction; human.
 screening; modulator; binding; neuropilin growth factor receptor;
 vascular endothelial growth factor C; vascular endothelial growth factor receptor 3; VBGP-C; VBGPR-3; neuropilin; cytostatic; nootropic; neuropicitve; vulnerary; vasotropic; cardiant; angiogenic process; nervous system growth; nervous system function; cancer; ischaemia; cerebral infarction;
 SEEABLLKLIEIGVOTGSTAQILQPDSGTTLSSPPV 1356
 SEEAELLKLIEIGVOTGSTAQILOPDSGTTLSSPPV 1356
 Z
 Human VEGFR-2 protein SEQ ID NO:30.
 standard; protein;
 WO2003029814-A2
 Homo sapiens
 01-JAN-2004
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 The present invention relates to novel antisense oligonucleotides (ACC71728-ACC71750 and ACC80101-ACC80155) targeted to Vascular Endothelial Growth Factor Receptor-2 (VEGFR-2) nucleotide sequence, and which inhibit the expression of VEGFR-2. The oligonucleotides are useful in compositions for treating a disease or condition associated with VEGFR -2, such as hyperproliferative disorder, e.g. cancer, a disease or condition involving angiogenesis, or rheumatoid arthritis. The present sequence is human VEGFR-2
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 New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding vascular endothelial growth factor receptor-2 (VEGFR-2), useful for treating a disease/condition associated with VEGFR-
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 PVCKNLDTLWKLNATWFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 WLWPINNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYQD
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 DOGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 EIKWYKNGI PLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 EIKWYKNGIPLESNHTIKAGHVLIIMEVSERDIGNYTVILINPISKEKOSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHHHWYWQLEEECANEPSQAVSVTNPY
 PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 RVISFHYTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
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 0; Indels
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 Score 7092;
Pred: No. 0;
 Example 13; Page 90-97; 127pp; English.
28-SEP-2001; 2001US-00967655
 99.98;
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 WPI; 2003-371980/35
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The present invention describes a method of screening for modulators of binding between a neuropilin growth factor receptor and a vascular endothelial growth factor (VEGF)—C or VEGFP—C or VEGFR—3 in the comparing the binding between neuropilin and VEGF—C or VEGFR—3 in the presence and in the absence of a putative modulator compound. Also described: (1) screening for selectivity of a modulator of VEGF-C, VEGFR—3 or neuropilin biological activity; (2) modulating growth, migration or proliferation of cells in a mammalian organism; (3) a bispecific antibody which specifically binds to a neuropilin receptor and a VEGFR—C or VEGFR—3 polypeptide; (4) modulating neuronal growth or neuronal scarring in a mammalian organism; and (5) a polypeptide comprising a fragment of a VEGFR—1 cthat binds to a neuropilin receptor. The modulators have cytostatic, noctropic, neuroprotective, vulnerary, vasciropic and cardiant activities. The method is useful in modulating angiogenic processes and certivities. The method is useful in modulating angiogenic processes and modulating system growth and function, such as in the treatment of cancer, wound, ischaemia, cerebral infarction/bleeding, Alzheimer's disease or myocardial infarction. The polypeptide comprising a fragment of a VEGFC container of a neuropilin receptor, is useful for manufacturing a very processes or that binds to a neuropilin receptor, is useful for manufacturing a
 in
 Screening for modulators of neuropilin and vascular endothelial growth factor (VEGF)-C or VEGFR-3 interactions, comprises comparing interaction of neuropilin and VEGF-C or VEGFR-3 in the presence and absence of a
 medicament for the treatment of diseases characterised by aberrant growth, migration or proliferation of cells that express a neuropilin receptor. The present sequence represents human VEGFR-2, which is used
 the exemplification of the present invention
 Disclosure; SEQ ID NO 30; 181pp; English
 Karila K;
 LUDWIG INST CANCER RES
LICENTIA LTD.
 01-OCT-2002; 2002WO-EP011069.
 01-OCT-2001; 2001US-0326326P
 Alitalo K, Karkkainen M,
 WPI; 2003-381660/36.
N-PSDB; ADD08953.
 modulator compound
 Sequence 1356 AA;
10-APR-2003
 receptor.
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 YRSPFIASVSDOHGVVYITENKOKTVVIPCLGSISNINVSLCARYPEKRFVPDGNRISWD
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVGYRIYDVVLSPSHGIELSVGE
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRI PAKYLGYPPP
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVARGSGMESLVEATVGERVRIPAKYLGYPPP
 Gaps
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Length 1356;
 Indels
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 DB
; Score 7092; DE; Pred. No. 0; 1; Mismatches
99.98;
Query Match
Best Local Similarity 99.9
Matches 1355; Conservative
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 RRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020
 1140
 1081 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML 1140
 420
 480
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 540
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 940
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 720
 780
 780
 840
 900
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK 960
 960
 361 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 LLVI ILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEPPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHHHWYWQLEEECANEPSQAVSVTNPY
 721 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 PCEEWRSVEDFOGGNKIEVNKNOFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 PCEEWRSVEDFQGGNKIEVNKROQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLODOGDYVCLAODRKTKKRHCVVRQLT
 601 PVCKNLDTLWKLNATWFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCYVRQLT
 661 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMMFKDNETLVEDSGIVLKDGRR
 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 GWVLASEELKTLEDRTKLSPSFGGWVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 LLVI I LRTVKRANGGELKTGYLS I VMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 GMVLASEELKTLEDRIKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 CMEEE EVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 SEEAELLKLIEIGVOTGSTAQILQPDSGTTLSSPPV 1356
 SEEAELLKLIEIGVOTGSTAQILOPDSGTTLSSPPV 1356
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 VYTI QSDVWSFGVLLWEI FSLGASPYPGVKI DEBFCRRLKEGTRMRAPDYTTPEMYQTML
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 PVCKNLDTLWKLNATWFSNSTNDILIMBLKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 LLVIILETVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 GRGAFGQVIEADAFGIDKTATCRTVAVKALKEGATHSEHRALMSELKILIHIGHHLAVVN
 LLGACTKPGGPLMVI VEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGA I PVDLK
 RRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 RRLDS I TSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLI CYSFQVAKGMEFLA
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 SRKCI HRDLAARNI LLSEKOVVKI CDFGLARD I YKDPDYVRKGDARLPLKMMAPETI FDR
 SRKCI HEDLAARNI LLSEKNVVKI CDFGLARDI YKDPDYVRKGDARLPLKWAAPETI FDR
 DCWHGEPSQRPTFSELVEHLGNLLQANAQOGKDYIVLPISETLSMEEDSGLSLPTSPVS
 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 RVI SFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 LIVIILRTVRRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEBFCRRLKEGTRMRAPDYTTPEMYQTML
 GWYLASEELKTLEDRIKLSPSFGGWVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
EIKWYKNGI PLESNHTIKAGHVLTIMEVSERDTGNYTVI LTNPI SKEKOSHVVSLVVYVP
 PCEEWRSVEDFQGGNXI EVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV
 SEEAELLKLIEIGVOTGSTAQILQPDSGTTLSSPPV
 ADF45097 standard; protein; 1356
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 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 240
 WINDOSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 120
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWD 180
 300
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEWKKFLSTLTIDGVTRS 300
 DOGLYTCAASSGLMTKKNSTFVRVHEXPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360
 The present sequence is the protein sequence of human vascular endothelial growth factor receptor-2 (VEGFR2 or KDR). A claimed DNA vaccine effective for eliciting an immune response against proliferating endothelial cells comprises a DNA construct operably encoding a VEGF receptor protein (e.g. KDR) in a carrier. The DNA construct may be a naked DNA construct or incorporated into a plasmid vector or into an attenuated bacterial vector such as attenuated Salmonella typhimurium. The DNA vaccine is used in claimed methods of inhibiting endothelial cell proliferation, inhibiting angiogenesis, and inhibiting tumour growth
 9
 New DNA vaccine for eliciting an immune response against proliferating endothelial cells comprising a DNA construct operably encoding a VEGF receptor protein in a carrier, useful for inhibiting tumor growth or anglogenesis.
 WLWPINIQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 Gaps
 Human; vascular endothelial growth factor receptor-2; VEGFR-2; KDR receptor; vaccine; genetic immunisation; gene therapy; cytostatic.
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 Length 1356;
 0; Indels
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 Score 7092; DF; DF; Pred. No. 0; 1; Mismatches
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 Claim 3; Fig 2; 56pp; English
 28-FEB-2003; 2003WO-US006256
 02-MAR-2002; 2002US-00090183
 99.9%;
 Reisfeld RA, Niethammer AG,
 (first entry)
 Query Match
Best Local Similarity 99.9
Matches 1355; Conservative
 WPI; 2003-756753/71.
N-PSDB; ACF80601.
 (SCRI) SCRIPPS RES
 Sequence 1356 AA;
 WO2003073995-A2.
 sapiens
 Human VEGF
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 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHHHWWQLEECANEPSQAVSVTNPY
 LLVI ILRTVKRANGGELKTGYLS I VMDPDEL PLDEHCERL PYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHIGHHLANVVN
 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
 PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 LLVIILRTVRRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKMMAPETIFDR
 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 CMEEBEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 1201 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 GMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNOTSGYOSGYHSDDTDTTVYS
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 standard; protein; 1356
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 The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that the present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
 YRSPFIASVSDQHGVVYITENRAKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWD
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 KLVLNCTARTELNVGI DFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 Gaps
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 Length 1356;
 0; Indels
 DB 7;
 enzyme; inhibitor; VEGFR2
 Score 7092; DE; Pred. No. 0; 1; Mismatches
 Disclosure; SEQ ID NO 66; 260pp; English.
 99.98;
 20-MAR-2003; 2003WO-US008725
 2002US-0366892P
 (SUNE-) SUNESIS PHARM INC
 Conservative
 Human; protein kinase;
 Braisted
 (first
 WPI; 2003-865136/80
 VEGFR2
 Query Match
Best Local Similarity
Matches 1355; Conserv
 Sequence 1356 AA
 WO2003081210-A2
 Human kinase
 Prescott JC,
 sapiens
 02-OCT-2003
 ADF45097;
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SKKGFTIPSYMISYAGMVPCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 240
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 541
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 601
 601
 199
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 721
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 781
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 841
 901
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 The invention relates to a novel method for determining whether a test compound inhibits tyrosine kinase activity in a mammal comprising measuring in the mammal the level of at least one of the proteins and/or mRNA transcriptor genes for such proteins comprising type 1 plasminogen activator inhibitor (PAI-1), TIMP-1 (tissue inhibitor of metalloproteinase 1), vinculin, vascular endothelial growth factor (VEGF), placental growth factor (WEGF), placental growth factor (MIG), exposing the mammal to the test compound and then measuring in the mammal the level of at least one of the proteins and/or mRNA transcripts previously measured. The method of the invention may be useful to determining whether a test compound inhibits tyrosine kinase activity in a mammal. The current sequence is that of the tyrosine kinase activity inhibition-related protein of the
 Determining whether a test compound inhibits tyrosine kinase activity in a mammal by exposing the mammal to the test compound and measuring in the mammal the level of at least one of the measured proteins or mRNA
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWD 180
 SKKGFTIPSYMISYAGAVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 240
 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 120
 120
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD 180
 9
 WIWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 protein.
 Gaps
 tyrosine kinase activity; type 1 plasminogen activator inhibitor; ETMP-1; tissue inhibitor of metalloproteinase 1; vinculin; vascular endothelial growth factor; VBGF; placental growth factor; migration inhibitory factor; MIG; human; vascular endothelial growth factor receptor 2; VBGFR2; receptor.
 Manning WC;
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 Human vascular endothelial growth factor receptor 2 (VEGFR2)
 8; Length 1356;
 0; Indels
 Smolich BD, J;
 B
 1; Mismatches
 99.9%; Score 7092; 99.9%; Pred. No. 0;
 Disclosure; SEQ ID NO 129; 408pp; English
 O'farrell A,
, Cherrington
 17-MAY-2002; 2002US-0380872P.
24-FEB-2003; 2003US-0448874P.
24-FEB-2003; 2003US-0448922P.
 19-MAY-2003; 2003WO-US015711
 (first entry)
 Conservative
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 Schilling
 Deprimo
 WPI; 2004-042604/04.
 Best Local Similarity
Matches 1355; Conserv
 (SUGE-) SUGEN INC
 Sequence 1356 AA;
 NO2003097854-A2
 Homo sapiens
 transcripts.
 11-MAR-2004
 Morimoto A,
 27-NOV-2003
 Walter SA,
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 Query Match
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1080 1200 1260 1320 SRKCIHEDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMADETIFDR 1080 VYIIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML 1140 1200 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML 1140 540 9 RRLDSITSSOSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020 420 480 480 540 9 9 9 720 780 960 LIGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK 960 300 360 420 720 780 840 840 GRGAFGQVIEADAFGIDKTATCRTVAVKWLKEGATHSEHRALMSELKILLIHIGHHLNVVN 900 300 ILVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL BIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS PQIGEXSLISPVDSYQYGTTQTLTCTVYAIPPPHHHHWYWQLEECANEPSQAVSVTNPY RVISPHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT PVCKNLDTLWKLNATWFSNSTND1L1MELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK DCWHGEPSQRPTFSELVEHLGNLLQANAQOGKDYIVLPISETLSMEEDSGLSLPTSPVS DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP EI KWYKNGI PLESNHTI KAGHVLTIMEVSERDTGNYTVI LTNPI SKEKOSHVVSLVVYVP PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY PCEEWRSVEDFQGGNK1EVNKNQFAL1EGKNKTVSTLV1QAANVSALYKCEAVNKVGRGE LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTPEDIPLEEPEVKVIPDDNQTDS GMVLASEELKTLEDRIKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTTVYS GWVLASEELKTLEDRTKLSPSFGGWVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS

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Sequence 1356 AA;

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Human myocardial infarction-associated gene derived protein, SEQ ID 1469.
 Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in
 Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human.
SEEAELLKLIEIGVOTGSTAQILQPDSGTTLSSPPV 1356
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 Claim 10; SEQ ID NO 1469; 145pp; English.
 Iakoubova 0;
 ADQ39806 standard; protein; 1356 AA
 myocardial infarction by detect
the individual's nucleic acids.
 20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
 22-DEC-2003; 2003WO-US040978
 (first entry)
 Cargill M, Devlin JJ,
 (APPL-) APPLERA CORP
 WPI; 2004-533949/51.
 N-PSDB; ADQ38978
 WO2004058052-A2
 Homo sapiens
 18-NOV-2004
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 961 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020
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 61 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVXVQD 120
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 1 MQSKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 241 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 WLWPINIQSGSEQRVEVTECSDGLFCKTLT1PKVIGNDTGAYKCFYRETDLASVIYVYVQD
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD
 SKKGFTI PSYMISYAGMVFCEAKINDESYQSIMY IVVVVGYRI YDVVLSPSHGIELSVGE
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLT1DGVTRS
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRI PAKYLGYPPP
 DOGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
 PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 541 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 661 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 LLVIILETVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 901 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 RRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 PVCKNLDTLWKLNATWFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 PVCKNLDTLWKLNATMFSNSTND1L1MELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
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 Score 7092; DE
Pred. No. 0;
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ilarity 99.9%;
Conservative
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Query Match
Best Local Simi:
Matches 1355;
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 The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single mucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's connected risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least contiguous nucleotides where one of the nucleotides is an SNP given in further comprision or its complement and encoding any one of the amino acid sequence given in the specification; an isolated polypeptide contains an amino acid sequence given in the specification; an antigen-binding comprising an amino acid sequence given in the specification and which is between about 16 and 1000 nucleotides in comprising an amplified polymucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in concluding an SNP in a nucleic acid molecule; and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a nucleic acids of the invention may be used in gene therapy. The nucleic acids of the invention may be used in gene therapy. The nucleic acids of the invention may be used in gene therapy. The composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction. This sequence was not shown in the specification. The sequence has come from a electronic sequence listing downloaded from the NIPO website.
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Sequence 1356 AA;
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 The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 Human myocardial infarction-associated gene derived protein, SEQ ID 1471.
 ij
 VYTI QSDVWSFGVLLWEI FSLGAS PYPGVKI DEEFCRRLKEGTRWRA PDYTTPEMYQTML
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKYIPDDNQTDS
 VYTIQSDVWSFGVLLWEIPSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 CMEBEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 GMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTTVYS
 Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism
 detection; single nucleotide polymorphism;
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV
 Claim 10; SEQ ID NO 1471; 145pp; English.
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 Iakoubova
 ADQ39808 standard; protein; 1356
 the individual's nucleic acids.
 cardiant; gene therapy; human.
 10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
 22-DEC-2003; 2003WO-US040978.
 (first entry)
 Myocardial infarction;
 Cargill M, Devlin JJ,
 (APPL-) APPLERA CORP
 WPI; 2004-533949/51.
 N-PSDB; ADQ38980
 WO2004058052-A2
 20-DEC-2002;
 Homo sapiens
 18-NOV-2004
 15-JUL-2004
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the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specification amino acid sequence given in the specification and which is between about 16 and 1000 nucleotides in the specification and which is between about 16 and 1000 nucleotides in the length; a kit for detecting an SNP in a nucleic acid, comprising the polymucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a mucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing:

The nucleic acids of the invention may be used in gene therapy. The myocardial infarction. The novel detection method has cardiant activity.

The nucleic acids of the invention may be used in gene therapy. The appropriate is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction. Note: This sequence was not shown in the specification. The sequence has come from a electronic sequence listing downloaded from the MIPO website. 480 480 54 Q 180 240 240 300 360 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360 420 120 420 540 9 9 99 9 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR 720 661 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFXDNETLVEDSGIVLXDGNR 720 WIMPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 120 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300 9 9 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 181 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE **EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP** PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE PCEEWRSVEDFOGGNKIEVNKNOPALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD KLVLNCTARTELNVG1DFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLT1DGVTRS DOGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY POIGEKSLISPVDSYOYGTTOTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT Gaps ö Score 7092; DB 8; Length 1356; Pred. No. 0; 1; Mismatches 0; Indels 0 99.06 Matches 1355; Conservative Local Similarity

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The present invention relates to a method for detecting cancer in a patient. The method comprises detecting in a biological sample from the patient a nucleotide or protein sequence comprising a sequence that is at least 80% identical to a nucleotide sequence (ADR4658-ADR46645) or protein sequence (ADR46646-ADR46703). The method is useful for detecting cancer for preparing a composition for diagnosing or treating cancer.
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD 180
 YRSPFIASVSDQHGVVYITENKAKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWD 180
 Detecting a pathological cell in a patient for diagnosing or treating cancer by detecting in a biological sample from the patient genes whose expression are up-regulated or down-regulated in specific cancers.
 WLWPINIQSGSEQRVEVTECSDGLFCKTLT1PKVIGNDTGAYKCFYRETDLASV1YVYVQD
 61 WIWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD
 301 DQGLYTCAASSGLMIXKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 SKKGFTI PSYMISYAGMVFCEAKINDESYQSIMYIVVVGYRIYDVVLSPSHGIELSVGE
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFF1IEGAQEKTNLEIIILVGTAVIAMFFWL
 361 EIKMYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP
 PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 PCEEWRSVEDFOGGNKIEVNKNOFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 RVISFHVTRGPEITLOPDMOPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 541 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVBATVGERVRIPAKYLGYPPP
 EIKWYKNGI PLESNHTI KAGHVLTIMEVSERDTGNYTVI LTNPI SKEKQSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEECANEPSQAVSVTNPY
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 Score 7092;
Pred. No. 0;
 Claim 1; SEQ ID NO 61; 375pp; English.
 expression are up-regulated or
 99.98;
 Query Match
Best Local Similarity 99.9
Matches 1355; Conservative
 Sequence 1356 AA;
N-PSDB; ADR46590
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 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKGGATHSEHRALMSELKILIHIGHHLNVVN
 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 NLTIRRVRKEDEGLYTCQACSVLGCAKVBAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 GRGAFGQVIEADAFGIDKTATCRTVAVKALKEGATHSEHRALMSELKILIHIGHHLNVVN
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 SRKCIHRDLAARNILLSEKAVVKICDFGLARDIYKDPDYVRKGDARLPLKWAAPETIFDR
 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEFEFEVKVIPDDNQTDS
 GWVLASEELKTLEDRTKLSPSFGGWVPSKSRESVASEGSNQTSGYQSGYHSDDTTVYS
 LIVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 RRIDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKMMAPETIFDR
 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 GWYLASEELKTLEDRIKLSPSFGGWVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
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 standard;
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 Cancer-associated
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 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDVVRKGDARLFLKWAPETIFDR
 VYTIQSDVWSPGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRWRAPDYTTPEMYQTML
 DCWHGEPSQRPTPSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 DCWHGEPSQRPTFSELVEHLGAILLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 CMEBEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVI PDDNQTDS
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
 SERAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
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Human vascular endothelial growth factor receptor 2 (VEGFR2) protein vascular endothelial growth factor receptor; VEGFR; protein co-ordinate data; X-ray diffraction; rational drug design; VEGFR2. Ą. standard; protein; 1356 (first entry) WO2004092217-A1 Homo sapiens ADT92353 ADT92353 RESULT 12 ADT92353 

Pinko Palmer CL, Mctigue MA, 17-APR-2003; 2003US-0463957P 05-APR-2004; 2004WO-IB001251 Kania RS, (PFIZ ) PFIZER INC Wickersham J; 28-OCT-2004 Bender

WPI; 2004-784574/77. N-PSDB; ADT92352.

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This invention relates to the novel crystalline structure of a vascular endothelial growth factor receptor (VEGFR) peptide-ligand complex, where the protein co-ordinate data is provided. Specifically, it refers to using X-ray diffraction techniques to provide structural information about the VEGFR kinase domain (VEGFRKD) and identify a ligand binding pocket and activation loop as defined in the specification. The present invention describes using this information to identify potential VEGFR modulators, as well as designing potential modulators using rational drug design and the three-dimensional structural information that will be able to bind to and modulate the activity of this protein. In particular, it identifies potentially important atoms and contributory amino acids by ansing root mean square deviation to highlight atoms that are within 1.25 Angstroms of the Invention. 240 240 300 120 121 YRSPFIASYSDQHGVYZITENKNKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWD 180 180 241 KLVLNCTARTELAVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300 360 301 DQGLYTCAASSGLMTKKXSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360 WIMPINGSGSEORVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 120 9 9 PCEEMRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE 181 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE KLYLNCTARTELAVGIDFNWEYPSSKHOHKKLVNRDLKTOSGSEMKKFLSTLTIDGVTRS 61 WLWPINNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD EIKWYKNGI PLESNHTI KAGHVLTIMEVSERDTGNYTVILTNPI SKEKQSHVVSLVVYVP Crystalline structure for identifying potential vascular endothelial growth factor receptor (VEGFR) modulator, of VEGFR peptide and ligand 1 MESKVILLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVGYRIYDVVLSPSHGIELSVGE DOGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP EIKWYKNGI PLESNHTI KAGHVLTIMEVSERDTGNYTVILTNPI SKEKQSHVVSLVVYVP POIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY RVISFHYTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT Gaps ö Score 7092; DB 8; Length 1356; Pred. No. 0; 1; Mismatches 0; Indels 0 Claim 4; SEQ ID NO 2; 332pp; English 99.98; Best Local Similarity 99.9 Matches 1355, Conservative Sequence 1356 AA; 61 421 Query Match 181 241 301 361 361 421 481 481 541 complex. ઠે 셤 ઠે ద 8 유 ò 셤 è g 8 셤 ò 유 8 셤 à 셤 8

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 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML 1140
 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS 1200
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK 960
661 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR 720
 GRGAFGQVIBADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLINVVN
 RRLDSITSSOSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWAPETIFDR
 VYIIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKGGTRMRAPDYITPEMYQTML
 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEFEFEVKVIPDDNQTDS
 GWVLASEELKTLEDRTKLSPSFGGWVPSKSRESVASEGSNQTSGYQSGYHSDDTTVYS
 LLVIILRTVKRANGGELKTGYLSIVMDPDBLPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVN
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
 CMEREEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
 GMVLASEELKTLEDRIKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
 SEEAELLKLIBIGVQTGSTAQILQPDSGTTLSSPPV 1356
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 Protease-hydrolysed polypeptide #62.
 ADV90285 standard; protein; 1356
 (first entry)
 10-MAR-2005
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 1321
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 ADV90285;
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Proteases with defined specificity for a target substrate useful for treating a specific disease related to the target substrate, such as cancer, asthma, diabetes, inflammatory disorders and psoriasis.

Claim 50; SEQ ID NO 115; 250pp; English.

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Voetsmeier

Scheidig A,

Koltermann A,

Haupts

WPI; 2005-057985/06.

2003EP-00025851, 2003EP-00025871, 2003EP-00013819

11-FEB-2004; 2004EP-00003058 (DIRE-) DIREVO BIOTECH AG

18-JUN-2004; 2004WO-EP051173

18-JUN-2003; 10-NOV-2003; 11-NOV-2003;

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Protease; immune disorder; inflammation; musculoskeletal disease; dermatological disease; gastrointestinal disease; endocrine disease; metabolic disorder; cancer; hematological disease; cardiovascular disease; neurological disease; growth disorder; respiratory disease; genitourinary disease; gynecological disorder; nutritional disorder; infection; cytostatic; gastrointestinal-gen,; antinflammatory; antiasthmatic; analgesic; antiarthritic; osteopathic; antidiabetic; nephrotropic; cardiovascular-gen,; immunosuppressive; respiratory-gen,; antipsoriatic; antiallergic; dermatological; enzyme; hydrolysis.
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WO2004113522-A1

29-DEC-2004

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The invention relates to the use of a protease with defined specificity for a target substrate for preparing a medicament for the treatment of a specific disease related to the target substrate. The invention also relates to a pharmaceutical or diagnostic composition comprising one or relates to a pharmaceutical or diagnostic composition comprising one or diagnostically acceptable carriers, excipients and/or auxiliary agents, contacting the target substrate in vivo or in vitro comprising contacting the target substrate with a protease as cited in the use mentioned, and a method for treatment of a disease in a patient connected with a specific target substrate comprising administering to the patient a protease with defined specificity for the specific target substrate or reduces or more biological activities, physico-chemical properties or her patient a protease hydrolyzes the target substrate and eliminates or reduces one or more biological activities, physico-chemical properties or increases one or more biological activities, physico-chemical properties or increases one or more biological activities, physico-chemical properties or the target protein, and/or adds one or or pharmacological activities of the target protein, and/or adds one or more biological activities of the target protein. The protease may be administered to treat immune disorders, inflammatory disorders, nematological diseases, cardiovascular diseases, neurological diseases, neurological diseases, cardiovascular diseases, neurological diseases, neurological diseases, cardiovascular diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, cardiovascular diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases, neurological diseases
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 241 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKCLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300
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 61 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD
 241 KLVLNCTARTELAVGIDFNWEYPSSKHOHKKLVARDLKTOSGSEMKKFLSTLTIDGVTRS
 1 MOSKVILAVALWICVETRAASVGIPSVSLDIPRISIOKDILTIKANTTLQITCRGORDID
 61 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD
 181 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 SKKGFIIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
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Best Local Similarity 99.9
Matches 1355, Conservative
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 GWVLASEELKTLEDRTKLSPSFGGWVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS. 1320
 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML 1140
 DCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS 1200
 RRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020
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 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK 960
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 VYTI QSDVWSFGVLLWEI FSLGASPYPGVKI DEEFCRRLKEGTRMRAPDYTTPEMYQTML
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMBSLVEATVGERVRIPAKYLGYPPP
 EIKWYKOKIPLESNHTIKAGHVLTIMEVSERDIGNYTVILTNPISKEKOSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHHHWYWQLEECANEPSQAVSVTNPY
 PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPTHVGELPT
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
 SRKCIHEDLAARNILLSEKNVVKICDPGLARDIYKDPDYVRKGDARLPLKWAAPETIFDR
 CMEEBEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 EIKWYKNGI PLESNHTI KAGHVLTIMEVSERDTGNYTVILTNPI SKEKQSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
 PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGOVI EADAFGI DKTATCRTVAVKMLKEGATHSEHRALMSELKI LI HI GHHLNVVN
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
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neovascularization, intraocular neovascularization, age related macular degeneration, corneal neovascularization, retinal neovascularization, choroidal neovascularization, diabetic retinal ischemia, or proliferative diabetic retinopathy. The present sequence represents a human VEGFR
 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 120
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD 180
 PDGF antagonist; VEGF antagonist; psoriasis; rheumatoid arthritis; age-related macular degeneration; antipsoriatic; dermatological disease; immune disorder; antiarthritic; antirtheumatic; immune disorder; inflammation; musculoskeletal disease; age related macular degeneration; ophthalmological; ocular disease; diabetic retinopathy; antidiabetic; ophthalmological; cardiovascular disease; ocular disease.
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 The invention relates to a method of treating a patient diagnosed with cat risk for developing a neovascular disorder, or suppressing a neovascular disorder in a patient. The method is useful for treating a patient diagnosed with or at risk for developing a neovascular disorder or suppressing a neovascular disorder, a patient. The neovascular disorder is an ocular neovascular disorder, is section to the match, irisk arthritis. The ocular neovascular disorder is ischemic retinopathy, irisk
 Treating an ocular neovascular disorder, comprises administering a platelet derived growth factor antagonist and a vascular endothelial growth factor antagonist, simultaneously or within ninety days of each
 1 MOSKVLLAVALMLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 1 MESKVILLAVALWICVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
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 9; Length 1356;
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 Score 7092; DE Pred. No. 0; 1; Mismatches
 Disclosure; SEQ ID NO 10; 112pp; English
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protein; 1356
 Adamis AP;
 26-AUG-2004; 2004WO-US027612
 27-AUG-2003; 2003US-0498407P.
26-MAR-2004; 2004US-0556837P.
 99.98;
 (EYET-) EYETECH PHARM INC
 Best Local Similarity 99.9
Matches 1355; Conservative
 Calias P,
 WPI; 2005-214423/22
standard;
 Local Similarity
 Sequence 1356 AA;
 N-PSDB; ADY59384
 WO2005020972-A2.
 Human VEGFR-2
 Homo sapiens
 10-MAR-2005
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 121
 121
ADY59385
 ADY59385
 Shima D,
 Query Match
 protein.
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The invention relates to a method of detecting lineage-specific cells in a biological sample which comprises identifying lineage-specific mRNA in the sample. The methods are useful for determining the clinical outcome of a progenitor cell transfer in a subject, and for identifying or quantifying lineage-specific cells. The present sequence represents the amino acid sequence of a human protein used to identify lineage-specific
MESKVILAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD
 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVGYRIYDVVLSPSHGIELSVGE
 Detecting lineage-specific cells in a biological sample, useful for determining the clinical outcome of a progenitor cell transfer in a subject, comprises identifying lineage-specific mRNA in the sample.
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Pred. No. 0;
1; Mismatches
 Disclosure, SEQ ID NO 187; 393pp; English.
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 (DAND) DANA FARBER CANCER INST
 cell; VEGFR2
 25-SEP-2003; 2003US-0506221P
08-OCT-2003; 2003US-0509594P
 24-SEP-2004; 2004WO-US031524
 Query Match
Best Local Similarity 99.9%;
Matches 1355; Conservative
 protein;
 WPI; 2005-273394/28.
N-PSDB; ADZ26560.
 standard;
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 Sequence 1356 AA
 WO2005030999-A1
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 culture;
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 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK 960
 SKKGFTIPSYMISYAGWVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTJDGVTRS
 EIKWYKNGI PLESNHTI KAGHVLTI MEVSERDTGNYTVI LTNPI SKEKQSHVVSLVVYVP
 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHHWYWQLEECANEPSQAVSVTNPY
 RVI SPHVTRGPEI TLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 GRGAFGQVIEADAFGIDKTATCRTVAVKWLKEGATHSEHRALMSELKILIHIGHHLNVVN
 LLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVDLK
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
 VYTI OSDVWS FGVLLWEI FSLGAS PY PGVKI DEE FCRRLKEGTRMRAPDYTTPEMYQTML
 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS
 DOGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP
 EIKWYKNGI PLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPI SKEKQSHVVSLVVYVP
 POIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY
 PCEEWRSVEDFQGGNKIEVNKNOFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILLHIGHHLNVVN
 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 VYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEFEFEVKVIPDDNQTDS
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL
 LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKMMAPETIFDR
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS
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Search completed: March 10, 2006, 18:26:46 fob time : 153.073 secs

ୁପସିତ Blauk (nebto)

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 10, 2006, 18:27:04; Search time 33.0732 Seconds (without alignments) 3944.887 Million cell updates/sec Run on:

US-10-633-742-6 7095 1 MESKVILAVALWILCVETRAA......GSTAQILQPDSGTTLSSPPV 1356 Perfect score: Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	protein-tyrosine k protein-tyrosine k	vascular endotheli	vascular endotheli	protein-tyrosine K	protein-tyrosine k	Fit-1 tyrosine kin	receptor tyrosine	embryonic receptor	platelet-derived g	platelet-derived g	platelet-derived g	platelet-derived g	macrophage colony-	platelet-derived g.	protein-tyrosine k	protein-tyrosine k	platelet-derived g	macrophage colony-	protein-tyrosine k	protein-tyrosine k	protein-tyrosine k	platelet-derived g	macrophage colony-	c-kit-related kina	protein-tyrosine k	fibroblast growth	fibroblast growth	⁻
SUMMARIES	JC1402 A41228	851656	JC4954	158375 A48999	S09982	I60598	178875	849010	PFHUGA	PFRTGA	533727	I51552 ·	T30816	T30815 .	A49814	JN0677	PFHUGB .	TVHUMD	TVMSKT	TVHUKT	I45877	PFMSRB	TVCTIMD	I51703	TVMVMD	TVCHFG	A49151	
% Query Match Length DB	1356 2	1348 2	1379 2	1363 2	1338 2	1336 2	1333 2	1330 2	1089 1	1088 1	1089 1	1087 2	975 2	1048 2	978 1	960 1	1106 1	972 P	975 1	976 1	977 2	1098 1	980 1	954 2	941 1	819 1	816 2	
* Query Match	99.6	70.9	42.0	20.00	38.7	37.3	37.0	36.2	17.2	16.8	16.7	15.9	15.7	15.3	15.0	14.9	14.9	14.8	14.6	14.6	14.4	14.3	14.3	14.1	14.0	13.9	13.9	
Score	7070	5031.5	2981.5	2804	2748.5	2648	2623.5	2570	1218.5	1189.5	1184	1131.5	1110.5	1085.5	1063	1057.5	1057.5	1052	1035	1034.5	1021	1018	1011.5	999.5	991.5	989.5	987.5	
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13.9	13.8	13.8	13.8	13.8	13.7	13.7	13.7	13.7	13.6	13.6	13.6	13.6	13.6	13.6
984	978	977.5	976.5	916	972	972	970	969.5	968	196	62	966.5	966.5	963.5

## ALIGNMENTS

RESULT 1 JC1402

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	protein-tyrosine kinase (EC 2.7.1.112) KDR - human	C
	C. Species: nome sapiests (mail)	8 #text change 05-0ct-2004
	C.Accession: JCI402: ISB357	שרכאר_ריימונאם סז-סנר-2004
	R; Terman, B.I.; Dougher-Vermazen, M.; Carrion, M.B.;	B.; Dimitrov, D.; Armellino, D.C.; Gospo
	Biochem. Biophys. Res. Commun. 187, 1579-1586, 199	
	A;itte: identification of the ADR Cylobine Ainabe as a A:Reference number: JC1402; MUID:93038639; PMID:1417831	receptor for Vascuiar
	A; Accession: JC1402	
	A, Status: nucleic acid sequence not shown	
	A;MOLECULE CYDE: MKNA A.Residues. 1-48 '1' 50-616 'E' 618-700 'E' 702-74	48.'F'.750-1263.'T'.1265-1290.'P'.1292-1
	A.Cross-references: UNIPROT: 935968; UNIPARC: UPI000017A3C3; EMBL:X61656; NID:931717	0017A3C3; EMBL:X61656; NID:g31717
	R; Terman, B.I.; Carrion, M.E.; Kovacs, E.; Rasmussen, B.A.; Eddy, R.L.;	sen, B.A.; Eddy, R.L.; Shows, T.B.
	Oncogene 6, 1677-1683, 1991	Charles and the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of th
	A; Ilcie: Idencillicación or a new endochellar cell growch A:Reference number: T58357: MITD:92019839: DMID:1656371	Tactor Teceptor
	A; Accession: I58357	
	A; Status: preliminary; translated from GB/EMBL/DDBJ	BJ
	A; Molecule type: mRNA	
	A; Kesidues: 3-1356 <tekz></tekz>	247: NID. 2186674: DIDN: AAA59459 1: DID:
	A)CIOSB-IELGIGGES: UNIFARCIOFIUOULEASSI; GB:DU4347; NID:91808/4; C:Comment: This enzyme acts as a receptor for vascular endothelial	
	C:Genetics:	
	A, Gene: GDB: KDR	
	A,Cross-references: GDB:127921; OMIM:191306	
•	A; Map position: 4012-4012	a nectoin. turnoing gascific arotoin kir
	F:766-790/Domain: transmembrane #status predicted	<pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre></pre> <pre>&lt;</pre>
	P,832-1167/Domain: protein kinase homology <kin></kin>	ų
	F;840-848/Region: procein Kinase Air-Dinding motif	-
	99.68;	2; Length 1356;
	Hest Local Similarity 99.5%; Fred. No. 5.28-285; Matches 1351; Conservative 1; Mismatches 4;	4; Indels 0; Gaps 0;
	Qy 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD	IQKDILTIKANTTLQITCRGQRDLD 60
	Db 1 MESKVLLAVALMICVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD	
	Qy 61 WLWPNNQSGSEQRVEVTECSDGLFCKTL/II PKVIGNDTGAYKCFYRETDLASVIYVYQD	NDTGAYKCFYRETDLASVIYVYVQD 120
	Db 61 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD	
	QY 121 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD	NLNVSLCARYPEKRFVPDGNRISWD 180
	Db 121 YRSPFIASVSDQHGVYYITENKNKTVVIPCLGSISNIAVSLCARYPEKRFVPDGNRISWD	
	Qy 181 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE	VVVVGYRIYDVVLSPSHGIELSVGE 240
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181 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVULSPSHGIELSVGE 240 241 KLVLNCTARTELMVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300 241 KLVLNCTARTELMVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300 301 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360 302 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360 303 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360 304 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGSRVRIPAKYLGYPPP 360 305 DGGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGSRVRIPAKYLGYPPP 360 306 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGSRVRIPAKYLGYPPP 360 421 EIKWYRNGIPLESNHTIKAGHVLITIMEVSERDTGNYTVILTNPISKERGSHVVSLVVVVP 420 422 PQGGEKSLISPVDSYQYGTTQTLCTVYALPPPHHHWYNQLEBECANESGANSVYTNPY 480 423 PQGGEKSLISPVDSYQYGTTQTLCTVYALPPHHHWYNQLEBECANESGANSVYTNPY 480 481 PCEEMRSVEDFQGGNKIEVNRNQFALIEGKNKTVSTLVTQAANSALYKCEAVNKVGRGE 540 482 PCEEMRSVEDFQGGNKIEVNRNQFALIEGKNKTVSTLVTQAANSALYKCEAVNKVGRGE 540 483 PCEEMRSVEDFQGGNKIEVNRNQFALIEGKNKTVSTLVTQAANSALYKCEAVNKVGRGE 540 484 PCEEMRSVEDFQGGNKIEVNRNQFALIEGKNKTVSTLVTQAANSALYKCEAVNRVGTE 560 485 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQLT 660 486 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQLT 660 487 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQLT 660 488 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQLT 660 489 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQLT 660 481 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQLT 660 481 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQLT 660 481 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQHT 660 481 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQHT 660 481 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQHT 660 481 PCKRLDTLMKLANATMESNSTNDILIMELKAASLODGGDYVCLAQDRKTKKRHCVVRQHT 660 481 LLVIILRRVAREDEGLYTCQACSVLGCAKVCRAGARPPPOINMFKNNETLVBESGTULKGRAFGOLIKGARAGGUKTATCTVANATMESGTUKTAANAGGELKTGYLLIMIN 790 481 GRGARGQVIREADAFGIDKTATCTVANATMEGGATHSEHRALMSELKTLLHIGHHNVN 900 481
41 KLVLNCTARTELNVGIDENWEYPSSKHOHKKLVNRDLKTOSGSEMKKFI  41 KLVLNCTARTELNVGIDENWEYPSSKHOHKKLVNRDLKTOSGSEMKKFI  41 KLVLNCTARTELNVGIDENWEYPSSKHOHKKLVNRDLKTOSGSEMKKFI  42 KLVLNCTARTELNVGIDENWEYPSSKHOHKKLVNRDLKTOSGSEMKKFI  43 KLVLNCTARTELNVGIDENWEYPSSKHOHKKLVNRDLKTOSGSEMKKFI  44 KLVLNCTARTELNVGIDENWEYPSSKHOHKKLVNRDLKTOSGSEMKKFI  45 CELENTAR TELNVGIDENWEYPSSKHOHKKLVNRDLKTOSGSENGERLYGERV  46 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTCNYTVILTNPISKEK  47 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTCNYTVILTNPISKEK  48 EIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTCNYTVILTNPISKEK  49 POLGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEECAN  40 POLGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEECAN  40 POLGEWRSVEDFOGGNKIEVNKNOPALIECKNKTVSTLVIQANVSALYI  41 RVISFHYTRGPEITLQPDMQPTEQESYSLMCTADRSTFENLTWYKLGP  42 RVISFHYTRGPEITLQPDMQPTEQESYSLMCTADRSTFENLTWYKLGP  43 RVISFHYTRGPEITLQPDMQPTEQESYSLMCTADRSTFENLTWYKLGP  44 RVISFHYTRGPEITLQPDMQPTEQESYSLMCTADRSTFENLTWYKLGP  45 LLILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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pecies: Mus musculus (house mouse)

te: 19-Jun-1992 #sequence revision 19-Jun-1992 #text_change 31-Dec-2004

coession: A41228; A46665; Issass, S18832; S29991

tithews, W.; Jordan, C.T.; Gavin, M.; Jenkins, N.A.; Copeland, N.G.; Lemischka, I.R.

Natl. Acad. Sci. U.S.A. 88, 9026-9030, 1991

title: A receptor tyrosine kinase cDNA isolated from a population of enriched primitive reference number: A41228; MUID:92020984; PMID:1717995
 seidues: 1-1367 <MAT.
coss-references: UNIPARC: UNIPARC: UPIO00002BD93; GB:X59397; NID:g50976; PIDN:C:
coss-references: UNIPARC: UNIPARC: UPIO00002BD93; GB:X59397; NID:g50976; PIDN:C:
coss-references: UNIPARC:
 tatus: preliminary; not compared with conceptual translation
olecule type: mRNA
esidues: 1-24,'T',26-782,'VL',785-916,'C',918-1367 <MIL>
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ross-references: UNIPARC:UPIO0003CA97; GB:X70842; NID:957923; PIDN:CAA50192.1; PID:95
ross-reference extracted from NCBI backbone (NCBIP:128064)
elrichs, R.B.; Reid, H.H.; Bernard, O.; Ziemiecki, A.; Wilks, A.F.
sygene B, 11-18, 1993
title: NYK/FLK-1: a putative receptor protein tyrosine kinase isolated from E10 embryor recession: I58365; MUID:93141255; PMID:8423988
 atus: preliminary; translated from GB/EMBL/DDBJ
lecule type: manNA
ducus: 1-678,'D',680-1340,'RSPPV' <OEL>
oss-references: UNIPARC:UPI0000170C47; GB:S53103; NID:g264004; PIDN:AAB25043.1; PID:g
 ywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transmembrane r
0-1165/Domain: protein kinase homology <KIN>
8-846/Region: protein kinase ATP-binding motif
 ein-tyrosine kinase (EC 2.7.1.112) Flk-1 precursor, endothelial cell-specific recepto
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 61 WIMPNAQRDSEERVLVTECGGGDSIFCKTLTIPRVVGNDTGAYKCSYRDVDIASTVYVYV 120
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 241 GEKLVINCTARTELNVGLDFTWHSPPSKSHHKKIVNRDVKPPPGTVAKMFLSTLTIESVT 300
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 179 WDSKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSV 238
 9
 9
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 DB 2; Length 1367;
 86.0%; Score 6100.5; DB 2; Length
85.7%; Pred. No. 1e-245;
Live 72; Mismatches 106; Indels
 1321 SEEAELLKLIEIGVQTGSTAQILQPDTGTTLSSPPV 1356
1321 SEEAELLKLIEIGVOTGSTAQILOPDSGTTLSSPPV 1356
 ches 1160; Conservative
 Similarity
 atus: preliminary
lecule type: mRNA
 ne: FLK-1; NYK
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 PTPVCKNLDTLWKLNATMPSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQ
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RESULT S51656

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A; Status: mucloic acid sequence not shown
A; Molecule type: mRNA
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A; Title: Two molecules calls a related to the VEGF receptor are expressed in early endothelial cof
A; Reference number: A56588; MUID: 93378866; PMID: 8396413
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A; Reference number: 150595; MUID: 940402; PMID: 1281306
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 57
vascular endothelial growth factor receptor 1 precursor - Japanese quail
N;Alternate names: quail endothelial kinase 1 (Quek 1); vascular endothelial
C;Species: Coturnix coturnix, aponica (Japanese quail)
C;Date: 07-May-1995 #sequence revision 01-Sep-1995 #text_change 05-Oct-2004
C;Accession: UC4953; A56598; Ī51162; S51656
R;Ricidmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996
A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial gr
 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
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 MVCSSEDTELL 1320
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C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 05-Oct-2004
C;Accession: JC4954
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996
A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor
A;Reference number: JC4953, MUID:97017121; PMID:8863722
A;Accession: JC4954
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
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A;Coss-references: UNIPARC:UP100000FD004; EMBL:X83287; NID:g619865; PIDN:CAA58267.1; PIL:
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 163 TWVPCLVSIPDLNVTLISQ--NSLIHPDRKTIFWDNKKGMQVPTQLIRDSLFVQCETVID
 DESYQSIMYIVVVGYRIYDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSS
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 338 EKPFINVEWRKGPV1EATAGDEAVKLPVKVVAYPQPDFQWYKAGKLIPKQSQSSMQ----
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JC4954
vascular endothelial growth factor receptor 2 precursor N;Alternate names: Quail endothelial kinase 2; Quek 2 C;Species: Coturnix coturnix japonica (Japanese quail)

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Length 1363; Indels 59 57 169

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-RSQSSALHPDGQEVLWDDRRGMRVPTQLLRDALYLQCETTWGDQNFLSNLFVVHITGNE 228
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 582 NYTYEHLRWYRLNLSTLHDAQGNPLLLDCKNV----HLFATPLEANLEEAEPGARHATLS 637
 747 KVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLSIVM
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 A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Cross-references: UNIPROT: P35917; UNIPARC: UP10000028D92; GB: L07296; NID: g293780; PIDN: R; Galland, F.; Karamysheva, A.; Mattel, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D. Genomics 13, 475-478, 1992
A; Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene. A; Reference number: A42010; MUID: 92307693; PMID: 1319394
A; Reference number: A42010; MUID: 92307693; PMID: 1319394
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A; Residues: 1033-1072 cGAL>
A; Cross-references: UNIPARC: UP1000017A423
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C;Species: 26-Jul-1996 #text_change 05-Oct-2004
C;Dace: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Oct-2004
C;Accession: I56375; B42010
R;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris, Oncogens 8, 1293-2298, 1993
A;Title: Molecular cloning of murine FLT and FLF4.
A;Title: Molecular cloning of murine FLT and FLF4.
A;Reference number: I58375; MUID:93330572; PMID:8393164
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 - mouse
 protein-tyrosine kinase (EC 2.7.1.112) flt4
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A;Cross-references: GDB:128732; OMIM:136352
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A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene. A;Title: Chromosomal NUID:92307693; PMID:1319394
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A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptua A;Molecule type: mRWA
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 163
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 688 CTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAK 747
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 SIPRVAPEHEGHYVCEVQDRRSHDKHCHKKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQ
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 463 WTPCKMFAORSLRRRQQQDLMPQCRDWRAVTTQDAVNPIESLDTWTEFVEGKNKTVSKLV
 519 IQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMQPTEQESVSLWCTADR
 576 STFENLTWYKLGPQPLPIHVGELPTPVCKNLDTLWKLNATMFSNSTNDI-----LIM
 ELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLTVLERVAPT1 TGNLENQTTSIGESIEVS
 EEEC----ANEPSQAVSVTNPYP-CEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLV
 344 VG-ERVRIPAKYLGYPPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTN
 403 PISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLJCTVYAIPPPHHIHWYWQL
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 79;
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 Indels
 5
 Query Match
38.8%; Score 2751.5; DB 2;
Best Local Similarity 44.9%; Pred. No. 7.4e-107;
Matches 597; Conservative 195; Mismatches 458;
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 submitted to the EMBL Data Library, December 1992
A;Reference number: 836130
A;Accession: 836130
A;Accession: 836130
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A;Residues: 1-23,'D',25-744,'P',746-751,'RP',754-889,'Q',891-1127,'V',1129-1145,'H',1147
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 ELIGDILQGGGWQEEEEERWALHSSQ--SSEEDGFWQASTTALHITEADADDSPPSWHCH 1224
 LKTLEDRIKLSPSFGGMVPSKSRESVASEGSNQ-----TSGYQSGYHSDDTDTTVYSSE 1322
 FEELESÄHRPEGSFSCKGPGQHMDIPRGHPDPQGRRRRPTQGAQGG-----KVFYNNE 1336
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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ILIAVALWICVETRAASVGLPSVSLDLPRLSIQXDILTIKANTTLQITCRGQRDLDWLWPN	300 KMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAFITVKHRKQQVLETVAGKRSYRLSMKV 359 355 LGYPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVLITNFISKEKQSHV 412 :	SEARCDFCSNNEESFILDADSNRGSNIISKAIIEGKNRAASILVANDSR VSALYKCEAVNKVGRGERVISFHVTRGPE-ITLQPDMQPTEQESVSLWCTADRSTFENLT	SGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAKVEA	871 KEGATHSEHRALMSELKILIHIGHHLAVVNLLGACTKPGGPLAVIVEFCKFGNLSTYLRS 930  864 KEGATASEYKALMTELKILTHIGHHLAVVNLLGACTKPGGPLAVIVEFCKFGNLSTYLKS 930  871 KRNEFVPYKTK-GARFRQGKDYVGAIPVDLKRRLDSITSSQSSASSGFVE 979  1
6 8 6 8 6 8 6 8 6	8 6 8 6 8 8 8	3 6 6 6 6 6	8 4 8 4 8 8 8	6 8 6 8 6 8 6
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	0.42 VKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL 1101	PDD GVE	nange 05-Oct-2004 A.; Matsushime, H.; an receptor-type tyro EMBL:X51602; NID:931	C;Genetics: A;Gene GDS:FLT1 A;Gene: GDB:120616; OMIM:165070 A;Map position: 13q12-13q12 C;Keywords: ATP; autophosphorylation; glycoprotein; membrane protein; phosphoprot C;Keywords: ATP; autophosphorylation; glycoprotein; membrane protein; phosphoprot F;1-22/Domain: signal sequence #status predicted <sig>F;1-23-1338/Product: protein kinase homology <kin>F;23-1338/Product: protein kinase homology <kin>F;825-1161/Domain: protein kinase homology <kin>F;833-841/Region: protein kinase ATP-binding motif Query Match Best Local Similarity 44.3%; pred. No. 1e-106; Matches 608; Conservative 212; Mismatches 436; Indels 115; Gaps 30;</kin></kin></kin></sig>

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K.; Merberg, D.M.; Kriz, R.; Morris, J.
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 947 QGKDYVGA-IPVDLKRRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHL 1005
 1000 ISYSFQVARGMEFLSSRKCIHRDLAARNILLSENNVVKICDFGLARDIYKNPDYVRRGDT 1059
 1060 RIPLKWMAPESIFDKVYSTKSDVWSYGVLLWEIFSLGGSPYPGVQMDEDFCSRLKEGMRM 1119
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C;Species: Mus musculus (house mouse)
C;Accession: 178875
R;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, F
Oncogene 8, 2293-2298, 1993
A;File: Molecular cloning of murine FLT and FLT4.
 -HPCHYNHSKERNDFCF
 -QGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRG
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 643 TGEE--ILRKTEVLVRDLEAPLLLQNLSDHEVSISGSTTLDCQARGVPAPQITWFKNNHK
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 ICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDA
 707 LVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEII
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 FCFSSCGHIRPVRQEDEDDP-----
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 C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Oct-2004
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C;Datesion: 160598
R;Yamane, A.; Seetharam, L.; Yamaguchi, S.; Gotoh, N.; Takahashi, T.; Neufeld, G.; Shibu Oncogene 9, 2683-2690, 1994
A;Title: A new communication system between hepatocytes and sinusoidal endothelial cells A;Reference number: 160598; MUID:94336223; PMID:8058332
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A;Accession: 160598
A;Accession: 160598
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 ||:
||ILINMAQANHTGLYSCRYLPKSTSKEKKMESAIYIFVSDAGSPFIEMHSDIPKLVHMTEG 151
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 | :| ||: |: |: |: |: || || :|| || ATVNGHLYQT-SYLTHRQTNTILDVQISPPSPVRFLRGQTLVINCTVTTDLNTRVQMSWN 267
 YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTF 321
 268 YPGKATKRASI---RQRIDQSNPHSNVFHSVLKINNVESRDKGLYTCRVKSGSSFRTFNTS 325
 VRVHEKPFVAFGSGMESLVEATVGERV-RIPAKYLGYPPPEIKWYKNGIPL--ESNHTIK 378
 435
 444
 436 QYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPYPCEEMRSVE--DF-- 491
 87
 91
 GISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDSGMVLASEELKTL---EDR
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 379 AGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVPPQIGEKSLISPVDS---Y
 Gaps
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Fit-1 tyrosine kinase receptor - rat
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 A;Cross-references: UNIPROT:P35969; UNIPARC:UP1000016CD30; EMBL:X78568; NID:9510664; PID:
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 138 ITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGM 197
 DASKWEFARERLKLGKSLGRGAFGKVVQASAFGIKKSPTCRTVAVKMLKEGATASEYKAL 876
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 MTEGRO----LIICRVTSPNVTVTL-KKFPFDTLTPDGQRITWDSRRGFIIANATYKEIGL 204
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C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Oct-2004
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 C;Accession: S49010
R;Choi, K.; Wall, C.; Hanratty, R.; Keller, G.
Oncogene 9, 1261-1266, 1994
A;Title: Isolation of a gene encoding a novel receptor t
A;Reference number: S49010; MUID:94181281; PMID:8134130
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 - mouse
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 645 QDRKTKKRHCVVRQLTVLER--VAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFK 702
 DASKWEFPRDRLKLGKPLGREAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRAL 882
 138 ITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGM 197
 VFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGEKLVLNCTARTELNVGID 257
 MSWNYPCKATKRASI -- RORIDRSHSHNNVFHSVLKINNVESRDKGLYTCRVKSGSSFQS 322
 318 NSTFVRVHEKPFVAFGSGMESLVEATVGER-VRIPAKYLGYPPPEIKWYKNGIP--LESN 374
 HTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVPPQIGEKSLISPVDS 434
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 595 -VGELPTPVCKNLDTLWKLNATMFSN-----STNDILI---MELKNASLQDQGDYVCLAR 644
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VPCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGEKLVLNCTARTELNVGID 257	HTIKAGHVLTIMEVSERDIGNYTVILTNPISKEKQSHVVSLVVYVPPOIGEKSLISPVDS 4	VGRGERVISFHYTRGPE-ITLOPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIH 59:	NETLYDDSGIVLKDGNRNLTIRRVKEDEGLYTCOACSVLGCAKVEAFFIIEGAGEKTN. 76	SELKILIHIGHHLAVVALLGACTKPGGPLAVIVEFCKFGALSTYLRSKRNEFVPXKTKGA 943	
198 VPCEAK;	375 HTIKAGI 381 RYLVHG) 435YQYC 440 PPLYPLC 490 DF	·	4 10 4 10 4 10	884 SELKILI 875 TELKILI 944 RFROGKU 935 HMELKKE 1003 EHLICKE 	1063 GDARLPI 1054 GDTRLPI 1123 TRWRAPD 1114 MRWRTPE 11183 TLSMEED 1172 ILTRNSN
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C;Comment: The extracellular domain is predicted to include five immunoglobulin-like doma
 AyMap position: 4g11-4g12
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology, C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology, C;Superfamily: Tyrosine-protein; giverited csign states and phosphorylation; dimer; glycoprotein; growth factor receptor; phosph F;25-1089/Product: platelet-derived growth factor receptor alpha #status predicted csign F;25-224/Domain: extracellular #status predicted csign contains immunoglobulin homology cimM1> F;42-102/Domain: immunoglobulin homology cimM2> F;428-503/Domain: immunoglobulin homology cimM3> F;428-504/Domain: immunoglobulin homology cimM3> F;528-548/Domain: immunoglobulin homology cimM3> F;528-548/Domain: intracellular #status predicted cimM> F;559-548/Domain: protein kinase homology ckinx> F;599-607/Region: protein kinase homology ckinx> F;599-607/Region: protein kinase homology ckinx> F;590-607/Region: protein kinase homology ckinx> F;42,76,103,179,353,359,458,468/Bainding site: carbohydrate (Asn) (covalent) #status predicted contain contains the carbohydrate (Asn) (covalent) #status predicted contains carbohydrate (Asn) (covalent) #status predicted contains carbohydrate car
 F;627/Active site: Lys #status predicted
F;849/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 ---SPNSTSMFEDYQLDTSTLLGSPLLKRFTWTETKPKASMKIDLRIASPRKEAGLSDLP 1285
1243 PLEEPEVKVIPDDNQTDSGMVLASEELKTL---EDRTKLSPSFGGMVPSKSRESVASEGS 1299
 44;
 117
 61 MSEEESSDVEIRNEENNSGLFVTVLEVSSASAAHTGLYTCYYNHTQTEENELEGRHIYIY 120
 118 VQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRI 177
 14 LLTGLSLILC------QLSLPSILPNENEKVVQLNSSFSLRCFGESEVSWQYP 60
 64
 platelet-derived growth factor receptor alpha precursor - human N;Contains: protein: tyrosine kinase (EC 2.7.1.112) (C.Species: Homo sapiens (man) (C.Species: Homo sapiens (man) (C.Species: 31-Dec-1992 #sequence_revision 31-Dec-1992 #squence_revision 1300 NQTSGYQSGYH----SDDTDTTVYSSEEAELLKLIEIGVQTGSTAQILQPDSGTTL--SS
 5 VLLAVALWICVETRAASVGLPSVSLDLPRISIQKDILTIKANTTLQITCRGQRDLDWLWP
 65 -NNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDL-----ASVIYVY
 Query Match
Best Local Similarity 25.8%; Pred. No. 2.3e-43;
Matches 370; Conservative 188; Mismatches 426; Indels 449; Gaps
 ••
 = ::
 A;Gene: GDB:PDGFRA
A;Cross-references: GDB:120267; OMIM:173490
 1354 PP 1355
 PP 1329
 A; Molecule type: mRNA
 1229
 1328
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us-10-633-742-6.rpr

qq	121 VPDPDVAFVPLGMTDYLVIVEDDDSAIIPCRTTDPETPVTLHNSEGVVPA 170	
È	. 178 SWDSKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHG 233	Ħ
QQ	:  ::    :   :   :   :   :   :   :   :	963
ò	234 IELSVGEKLVINCTARTELNVGIDFNWEYPSSKHOHKKLVNRDLKTQSGSEMK 286	1249
qq	216 LEMBALKTVYKSGETIVVTCAVFNNEVVDLQWTYPGEVKGKGITMLEEIKVPSI 269	· //6 ·
ò	287 KFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATV 344	201 YOUR TEACH AND THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
qa	270 KLVYTLTVPEATVKÖSÖDYECAARQATREVKEMKKVTISVHEKGFIEIKPTFSQLEAVNL 329	
ò	345 GERVRIPAKYLGYPPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDT 393	RESULT 12
q	330 HEVICHFUVEVRAYPPPRISWLKNNLTLIENLTEITTDVEKIQEIRYRSKLKLIRAKEEDS 389	platelet-derived g
ò	394 GNYTVILTNPISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIP 451	C; Species: Procest
qq	390 GHYTIVAQNEDAVKSYTFELLIQVPSSILDLVDDH-HGSTGGGTVRCTAEG 439	C; Accession: A3471
õ	452 PPHHIHWYWQLEEECANEPSQAVSVTNPYPCEEMRSVEDFQGGNKIEVNKNQFALIEGKN 511	Mol. Cell. Biol. 1
qa	440 454 454	A;Reference number
ઠે	512 KTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPEITLQPDMQPTEQESVSLWC 571	A,Status: nucleic
qo	455	A; Molecule Lype: III A; Residues: 1-1088
ò	572 TADRSTFENLTWYKLGPQPLPIHVGELPTPVCKNLDTLWKLNATWFSNSTNDILIMELKN 631	A;Cross-references A;Note: in the aut)
đ	457	Biochim. Biophys.
ò	632 ASLODOGDYVCLAQDRXTKKRHCVVRQLTVLERVAPTITGNLENQTTSIGESIEVSCT 689	A; iitie: Conservat A; Reference number
q	478SRDRST	A; Accession: 53376 A; Status: nucleic
ò	690 ASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDBGLYTCQACSVLGCAKVF 749	A; Molecule type: m A; Residues: 33-149
Ωp	503 AKNLIGAENRE 513	A; Cross-references A; Experimental sour
ò	750 AFFIIEGAQEKTNLEIILLYGTAVIAMFFWLLLVIILRTVKRANGGELKTG 800	Rinerren, B.; weyer submitted to the El
qq	514 LKLVAPTLRSELTVAAAVLV-LLVIVISLIVLVVIWKQKPRYEIRWRVIESISPDG 569	A;Reference number
ò	CPLDEHCERI	A; Molecule type: ml
셤	570 HEYIYVDPMQLPYDSRWEPPRDGLVLGSGAFGKVVEGTAYGLSRSQ 619	A; residues: 33-143 A; Cross-references
ò	861 TCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLAVVVNLLGACTKPGGPLMVIVEFCK 920	C; Superramily: 1yro C; Keywords: ATP; at
đ	620 PVMKVAVKMLKPTARSSEKQALMSELKIMTHLGPHLNIVNLLGACTK-SGPIYIITEYCF 678	F; 1-23/DOMAIN: BIG F; 24-1088/Product: E: 24-523/Domain: e
È	921 FGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVD 958	F;41-101/Domain: ir F:41-100/Domain: ir
qq	679 YGDLVNYLHKNRDSPLSHHPEKPKKBLDIFGLNPADESTRSYVILSFENNGDYMDMKQAD 738	F;227-291/Domain: F:427-502/Domain:
ò	959 LKRRLDSITSSQSSASSGFVBEKSLSDVEBEAPEDLYKDFLTLEHLICY 1008	F;524-547/Domain: F:548-1088/Domain:
qq	739 TTQYVPMLERKEVSKYSDIQRSLYDRPASYKKKSMLDSEVKNLLSDDNSEGLTLLDLLSF 798	F;590-956/Domain: PF:598-606/Region:
È	1009 SFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLP 1068	F;48-99,149-188,23
qq	799 TYQVARGMEFLASKNCVHRDLAARNVLLAQGKIVKICDFGLARDIMHDSNYVSKGSTFLP 858	F:626/Active site: F:848/Binding site
ò	1069 LKWMAPETIFDRVYILQSDVWSFGVLLWEIFSLGASPYPGVKIDEFCRRLKEGTRWRAP 1128	Ouery Match
q	859 VKWMAPESIFDNLYTTLSDVWSYGILLWEIFSLGGTPYPGMMVDSTFYNKIKSGYRMAKP 918	Best Local Simila Matches 369; Co
<b>&amp;</b> :	DYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEE	Oy 25 PSV-
a	919 DHATSEVYEIMVKCWNSEPEKRPSFYHLSEIVENLLPGQYKKSY 962	<u>.</u>
	Commence of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of th	Special Control

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growth factor receptor alpha precursor - rat
in-tyrosine kinase (BC 2.7.1.112)
sorvegizes (Norway rat)
922 #sequence revision 31-Dec-1992 #text_change 05-Oct-2004
710; S33767; $25100
710, S337-2246, 1990
10, 2237-2246, 1990
10, and characterization of the alpha platelet-derived growth factor receptor: A34710; MUID:90220609; PMID:2157969
 18 <LEE>
strong in Translation an additional residue, Val, is shown after position
ter, X.A.; Rouge, M.; Loetscher, P.; Pech, M.
Acta 1173, 294-302, 1993
 tion in sequence and affinity of human and rodent PDGF ligands and recert S33764; WUID:93305723; PMID:8318539
 49, 77, 151-518, 7T, 520-523 «HER1»
as: UNITARC:UPI00001709A&E; EMBL:Z14118; NID:g56863; PIDN:CAA78488.1; PID
ource: strain Sprague Dawley
ource: K.A.; Rouge, M.; Loetscher, P.; Pech, M.
PMBL Data Library, July 1992
coss-species conservation in sequence and function of PDGF ligands and r
zr: S25096
 The: mkWA

19-149, TK, 151-518, T', 520-523 (HER2>

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LSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPE 1248
 VIPDDNQTDSGMVLASEE--LKTLE---DRTKLSPSFGGMVPSKSRESVASE---- 1297
 45;
 ----- DHPA 976
 ---SEDEPRESIQKDILTIKANTTLQITCRGQRDLDWLWPNNQSGSEQRVEV--TEC 79
 16.8%; Score 1189.5; DB 1; Length 1088;
larity 26.2%; Pred. No. 3.6e-42;
Conservative 183; Mismatches 431; Indels 427; Gaps
 GSNQTSGYQSGYHSDDTDTTVYSSEEAELLKLIEIGVQTGSTAQILQPDS 1347
 -----EXIHID------FLKS------
 acid sequence not shown
 acid sequence not shown
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OY 1092 GVLLWEIPSLGASPYPGVKIDEEFCRRLKEGTRW DD 881 GVLLWEIFSLGGTPYPGWNUDSTFYNKIKSGYRW OY 1152 TFSELVEHLGNLLQANAQODGKDYIVLPISETLS	RESULT 13 S33172 plate1et-derived growth factor receptor alpha pr N;Contains: protein-tyrosine kinase (EC 2.7.1.11 C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-19 C;Accession: 157511; 833727 R;Stiles, C.D.; Wang, C. Mol. Cell. Biol. 10, 6781-6784, 1990 A;Title: Retinoic acid promotes transcription of A;Reference number: 157511; MUD:91061789; PMID: A;Reference number: 157511 A;Reference number: 157511 A;Genetics: Preliminary; translated from GB/EMBL/D A;Molecule type: mRNA A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Gene	Db 19
17 PSLIVCQLLLPSILPNENEKIVPLSSSFSIRCFGESEVSWQHPMSEE-EDPNVEIRTEEN 75  80 SDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVITVYVQDYRSPFI-ASVSDQ 132  1		
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of the platelet-derived growth factor alphe D:2174116
 I000016CF20; GB:M57683; NID:g199783; PIDN:#
 PDGF receptor type; immunoglobulin homology eceptor; phosphotransferase; transmembrane ed <SIG>
 otif
| site: carbohydrate (Asn) (covalent) #statı|
 LSMEEDSGLSLPTSPVSCMEEEEVCDPK 1211
 LEEPEV-KVIPDDNQTDSGMVLASEELK 1270
 RMRAPDYTTPEMYQTMLDCWHGEPSORP 1151
 PEKREVPDGNRISWDSKKGFTIPSYMIS 193
 TQSGSEMKKFLSTLTIDGVTRSDQGLYT 306
 -----EX 963
 : : :: ||:|| | SEIEGRHIYIYVPDPDMAFVPLGMTDSL 137
 WLSPSHGIEL-----SVGEKLVLNC 246
 ASV----IXVYVQDYRSPFI-ASVSDQH 133
 SSLVEATVGERVRIPAKYLGYPPPEIKW 364
 GQRDLDWLWPNNQSGSEQRVEV--TECS 80
 |: :: | | :: : | |: GESEVSWQHPMSEE-EDPNVEIRSEENN 77
 1999 #text_change 05-Oct-2004
 DB 1; Length 1089;
1e-42;
8 417; Indels 436; Gaps
 precursor - mouse
112)
 /DDBJ
 347
 980
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qa		d d	1054 SSSST-FIKREDETIEDIDMMDDIGIDSSDLVEDS 1087
රු සි	365 YKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVV 413	RESULT 151552 platele	14 tt-derived growth factor A receptor - African clawed frog
ò q	414 SLVVXVPPQIGEKSLISPVDSYQ-YGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQ 472	C,Species C,Date: 1 C,Accessi R,Jones,	C.)Species: Actions aggins (Allican Caswed 1789) (C.)Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004 C.)Accession: IS1552 R.Jones, S.D.; Ho, L.; Smith, J.C.; Yordan, C.; Stiles, C.D.; Mercola, M.
ò	VEDFQGGNK1 EVNKNQFAL I EGKNKTVSTLV1 QAANVSALYKCEA	Dev. Gene A;Title: ion.	Genet. 14, 185-193, 1993 le: The xenopus platelet-derived growth factor alpha receptor: cDNA cloning and dem
음 &	440GPLPEIDW 447 533 VNKVGRGERVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLP 592	A;Refer A;Acces A;Statu	A;Reference number: I51552; MUID:93365089; PMID:8358864 A;Accession: I51552 A;Status: preliminary; translated from GB/EMBL/DDBJ
<u>අ</u> දි	448MICKHIKK	A; Resid A; Cross	A;Molecule Lype: mana A;Residues: 1-1087 <jon> A;Conetine: Child (B: MID: 1080) WIPPARC: UPI0000131795; GB:M80798; NID:g214652; PIDN: Chicanetine:</jon>
<b>3</b> 43		A; Gene:	PDGFAR Farming Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
දු පු	653 HCVVRQLTVLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMMFKDNETLVEDSG 712	F;43-10 F;533-9 F;601-6	F;43-103/Domain: immunoglobulin homology <imm> F;593-957/Domain: protein kinase homology <kin> F;601-609/Region: protein kinase ATP-binding motif</kin></imm>
<u>ኞ</u> ብ	713 IVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTA 772 :	Query Best Match	Query Match 15.9%; Score 1131.5; DB 2; Length 1087; Best Local Similarity 25.2%; Pred. No. 9.2e-40; Matches 354; Conservative 187; Mismatches 390; Indels 475; Gaps 48;
රු සි	773 VIAMFFWLLLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYD 923 ::	<u>ک</u> م	31 LPRLSIQKDILTIKANTILQITCRGQRDLDWLWPNNQSGSBQRVEVTECSDGLFCKTL 88
ço g	824 ASKWEPPRDRLKLGKPLGRGAPGQVIEADAFGIDKTATCRTVAVRMLKEGATHSEHRALM 883  :	ος · αα	89 TIPKVIGNDTGAYKCFYRETDLASVIYVYVQDYRSPFIASVSDQHGVVYITENK 142
& d	884 SELKILIHIGHHLAVVNILGACTKPGGPLAVIVEFCKPGNLSTYLRSKRNEFVPYKT 940	ço da	143 NKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMV 198 ::::   :
දු දු	941 KGARFRQGKDYVGAIPVDLKRRLDSIISSQSSASSGFV 978 	ço,	199 FCEAKINDESYQSIMYIVVVGYRIYDVVLSPSHGIELSVGEKLVLNCTAR 249
රු සි	979EEKSLSDVEEEAPEDLYKDFLTLEHLICYSPQVAKGMEFLASRKCIH 1026 1:	oy De	250 TELANVGIDENWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLY 305
& g	1027 RDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYT1QS 1086	₽ Q	306 TCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPP 359  1
රු අ	1087 DVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRARAPDYTTPEMYQTMLDCWHGE 1146	<u>م</u> م	360 PEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEK 408 
& g	1147 PSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVSCMEEEE 1206   :  :	δ da	409 OSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEEC 466
è 6	1207 VCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEV-KVIPDDNQTDSGMYLA 1265 	λ d	467 ANEPSQAVSVTNPYPCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSA 526
8 1	1266 SEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSD 1312	8 1	LYKCEAVNKVGRGE
8 &	995 NEEDKLKUWEGGLDEQKLSAUSGYIIFLKUIDFVYEEEDLGKKKKKKSSQIS-EESAIEIG 1053 1313 DIDTIVYSSEEAELLKLIEIGVQTGSTAQILQPDS 1347	g &	S87 GPQPLPIHVGELPTPVCKNLDTLWKLNATWFSNSTNDILIMELKNASLQDQGDYVCLAQD 646
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	60BISMETHQDD	RKTKKRHCVVRQLTVLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDN	ETLVEDSGI VLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFI I EGAQEKTNLE :	IIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLSIVMDPDELPLDE ::   :	HCERLPYDASKWEFPRDRLKLGKPLGRGAFGQVIEADAPGIDKTATCRTVAVKMLKEGAT	HSEHRALMSELKILIHIGHHLAVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEF	VPYKTKGARFRQGKDYVGAI PVDLKRRLDSITSSQSSA	SSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFOVAKGMEPLASRK   ::	CIHRDLAARNILLSEKNVVKI CDFGLARDIYKDPDYVRKGDARLPLKWAAPETIFDRVYT  CIHIDIAARNILLSEKNVVKI CDFGLARDIYKDPDYVRKGDARLPLKWAAPETIFDRVYT  C'HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	IQSDVWSFGVLLWEIFSLGASPYFGVKIDEBFCRRLKEGTRMRAPDYTTPEMYQTMLDCM 	HGEPSQRPTFSELVEHLGNLLQANAQQDCKDYIVLPISETLSMEEDSGLSLP	TSPVSCMEEEEVCDPKFHYDNT-AGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPD	DNQTDSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDT 	DTTVYSSERABLLKLIEIGVQTGSTA    :    ::   ::	RESULT 15 T30816 macrophage colony-stimulating factor receptor - Japanese pufferfish	ប្	human	(7) €	<b>=</b>

768 QGLDFLASRNCIHRDVAARNVLLTDKRVAKICDFGLARDIMNDSNYVVKGNARLPVKMMA 827	1074 PETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEBFCKRLKEGTRWRAPDYTTP 1133	828 PESIFDCVYTVQSDVWSYGILLWEIFSLGKSPYPSMAVDSRFYKMVKRGYQMSQPDFALP 887	1134 EMYQTMLDCWHGEPSQRPTFSELVEHLGANAQQDGKDYIVLPISETLSMEEDSGLS 1193	888 BIYMIMKWCWNLEPTERPTESMISQMINRLLGGQDEQEKLIYRNVQPEQ 936	1194 LPTSPVSCMEREEVCDPKFHYD 1215	VAEGEACDEPKRYD 950	
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Search completed: March 10, 2006, 18:38:07 Job time : 44.0732 secs

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 DB 2; Length 1356;
 Sequence 2, Application US/09098707A

Sequence 2. Application US/09098707A

Patent No. 6204011

CENERAL INFORMATION:

APPLICANT: Kendall, Richard L.

Mao, Xianzhi

TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KOR

NUMBER OF SEQUENCES: 8
 CITY: Rahway
STATE: NJ
COUNTRY: NJ
COMPUTER: NJ
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tale PC compatible
COMPUTER: Tale PC compatible
COMPUTER: Tale PC compatible
COMPUTER: Tale PC compatible
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CLASSIFICATION NUMBER: 36,545
REGISTRATION NUMBER: 36,545
REFERENCE POCKET NUMBER: 36,545
REFERENCE POCKET NUMBER: 36,545
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REFERENCE POCKET NUMBER: 30,547
TELEPHONE: 732/594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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100.0%; Pred. No. 0;
ive 0; Mismatches
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 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
 TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 1356; Conservative
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 March 10, 2006, 18:36:34; Search time 33.7622 Seconds (without alignments) 3320.525 Million cell updates/sec
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US-09-142-956B-14
US-08-874-678-2
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Maximum Match 100%
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length: 2000000000
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 Length 1356;
 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTT
 Indels
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 APPLICANT: Kendall, Richard L.
APPLICANT: Thomas, Kenneth A.
APPLICANT: Thomas, Kenneth A.
APPLICANT: Teben, Andrew J.
TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE,
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
ADBRESSER: Merck & Co., Inc.
STREET: P.O. Box 2000
 STREET: P.O. BOX 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/483,539
FILING DATE:
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 DB 2;
 100.0%; Score 7095;
Similarity 100.0%; Pred. No. 0;
56; Conservative 0; Mismatches
 19963PV
 ; Sequence 2, Application US/09483539; Patent No. 6359115; GENERAL INFORMATION:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFRENCE/DOCKET NUMBER: 1996:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732/594-3905
 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
 LENGTH: 1356 amino acids
 Query Match
Best Local Similarity 100.
Matches 1356; Conservative
 732/594-4720
 STRANDEDNESS: single
 TYPE: amino acid
 TOPOLOGY: linear
 TELEFAX:
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US-09-483-539-2
 US-09-483-539-2
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 DB
 APPLICANT: Rondall, Richard L.
APPLICANT: Thomas, Kenneth A.
APPLICANT: Thomas, Kenneth A.
APPLICANT: Mod. Xiaizhi
APPLICANT: Thomas, Kenneth A.
APPLICANT: Tebben, Andrew
TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KIN
FILE REPRERENCE: 199637DC
CURRENT APPLICATION NUMBER: US/10/100,405A
CURRENT PILING DATE: 2002-08-13
PRIOR FILING DATE: 2001-12-18
PRIOR PELICATION NUMBER: 09/493,539
PRIOR PELICATION NUMBER: 09/493,539
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1997-06-18
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NUMBER: OF SEQ ID NOS: 8
NUMBER: FASELSEQ FOR WINDOWS VERSION 4.0
 100.0%; Score 7095;
100.0%; Pred. No. 0;
ive 0; Mismatches
 ; Sequence 2, Application US/10100405A; Patent No. 6841367; GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.0
Matches 1356; Conservative
 TYPE: PRT
ORGANISM: Human
 RESULT 3
US-10-100-405A-2
 US-10-100-405A-2
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 CURRENT APPLICATION NUMBER: US/10/022,939
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/483,539
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 09/098,707
PRIOR FILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR FILING DATE: 1997-06-18
NUMBER: OF SEQ ID NOS: 8
SEQ ID NO 2
 100.0%;
 Query Match
Best Local Similarity 100.
Matches 1356; Conservative
 ; TYPE: PRT
; ORGANISM: Human
US-10-022-939-2
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 Sequence 2, Application US/10022939
Fatent No. 6441382
GENERAL INFORMATION:
APPLICANT: Thomas, Kenneth A.
APPLICANT: Thomas, Kenneth A.
APPLICANT: Tabben, Andrew
APPLICANT: Tebben, Andrew
ITILE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
 SEEAELLKLIEIGVOTGSTAQILOPDSGTTLSSPPV 1356
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV
 RESULT 4
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120 120 180 YRSPFIASVSDQHGVVVITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD 180 240 240 300 300 360 360 420 480 480 540 540 900 900 720 720 780 780 420 999 99 9 1 MESKVILAVALWILCVETRAASVGLPSVSLDIPPILSIQKDILTIKANTTLQITCRGQRDLD 61 WIMPINNOSGSEORVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 61 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS KLVLNCTARTELNVGIDFNWEYPSSKHOHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS DOGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHHWYWQLEECANEPSQAVSVTNPY 541 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT PVCKNLDTLWKLNATWFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT VLERVAPTITGNLENQTISIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR EIKWYKNGI PLESNHTIKAGHVLTIMEVSERDTGNYTVI LTNPI SKEKQSHVVSLVVYVP PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY PCEEWRSVEDFQGGNKI EVNKNQFALI EGKNKTVSTLVI QAANVSALYKCEAVNKVGRGE **RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT** PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT

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 Sequence 6198, Application US/09949016
; Sequence 6198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PPLING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
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; Pred. No. 0;
1; Mismatches
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 Query Match
Best Local Similarity 99.9
Matches 1355; Conservative
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 ; ORGANISM: Huma:
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QY         421         PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEGCANEPSQAVSVTNPY 480           Db         521         PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEGCANEPSQAVSVTNPY 580           QY         481         PCEEWRSVEDPCQGGNKIEVNRYQFALIEGRNKTVSTLVIQAANVSALYKCEAVNKVGRGE 540           Db         581         PCEEWRSVEDPCQGGNKIEVNRYQFALIEGRNKTVSTLVIQAANVSALYKCEAVNKVGRGE 640           QY         541         RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT 600           GO         641         RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT 700           QY         601         PVCKNLDTLWKLNATWENSTRDILIMELKNASLQDQGDYVCLAQDRYTKKRHCVRRQLT 660           Db         701         PVCKNLDTLWKLNATWFSNSTRDILIMELKNASLQDQGDYVCLAQDRYTKKRHCVVRQLT 760           Db         701         PVCKNLDTLWKLNATWFSNSTRDILIMELKNASLQDQGDYVCLAQDRYTKKRHCVVRQLT 760	ENOTTS IGES IEVSCTASGNPPPOINMFENDETLY DESCIVILED ON THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE ST	US-08-8U-11b-8 Sequence 8, Application US/08810116 Patent No. 5766860 GENERAL INPORATION: APPLICANT: Terman, Bruce I.
Qy         1141 DCWHGEPSQRPTFSELVEHLGNLLQANAQODGKDYIVLPISETLSMEEDSGLSLPTSPVS 1200           Db         1141 DCWHGEPSQRPTFSELVEHLGALAQODGKDYIVLPISETLSMEEDSGLSLPTSPVS 1200           Qy         1201 CMEEEBVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEKKVIPPDDNQTDS 1260           Db         1201 CMEEEBVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEKKVIPPDDNQTDS 1260           Db         1201 CMEEEBVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPPDDNQTDS 1260           Qy         1261 GMVLASEBLKTLEDRTKLSPSFGGAVVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS 1320           Db         1261 GMVLASEBLKTLEDRTKLSPSFGGAVVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS 1320           Qy         1321 SBEABLLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356           Db         1321 SBEABLLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356           Db         1321 SBEABLLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356	PRESENT 6   10.00-0553   10.00-05-05-05   10.00-05-05-05-05   10.00-05-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05   10.00-05-05-05-05   10.00-05-05-05-05-05-05-05-05-05-05-05-05-0	DD 401 DGLYTCAASSGLMTKKNSTFVRVHEKPFVAESGMESLVERITHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR 1080
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 1201 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS 1260
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 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT
 a No. 5861301el Human Growth
 GENERAL INFORMATION:
APPLICANT: Terman, Bruce I.
APPLICANT: Carrion, Miguel E.
TITLE OF INVENTION: Identification of a N
TITLE OF INVENTION: Factor Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMERICAN CYANAMIC COMPANY
 ; Sequence 8, Application US/07930548A; Patent No. 5861301
 RESULT 8
US-07-930-548A-8
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 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVR1PAKYLGYPPP 360
 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAPGSGMESLVEATVGERVRIPAKYLGYPPP 360
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 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD 60
 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 Gaps
 of a No. 5766860el Human Growth
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 Length 1356;
 4; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 DB 1;
 99.6%; Score 7070; D
99.6%; Pred. No. 0;
iive 1; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/930,548
FILING DATE: 23-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REPERENCE/DOCKET NUMBER: 31,298-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TITLE OF INVENTION: Identification of TITLE OF INVENTION: Factor Receptor NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: American Cyanamid Company STREET: One Cyanamid Plaza CITY: Wayne STATE: New Jersey COUNTRY: U.S.A.
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,116
FILING DATE: 25-FEB-1997
 TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1356 amino acids
 Best Local Similarity 99.6
Matches 1351; Conservative
 ; MOLECULE TYPE: protein US-08-810-116-8
 amino acid
 FILING DATE: 2:
CLASSIFICATION:
 ZIP: 07470
 TYPE: ami
TOPOLOGY:
 361
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 1141 DCWHGEPSQRPTFSELVEHLGNLLQANAQOGKDYIVLPISETLSMEEDSGLSLPTSPVS 1200
 1320
 RRLDSITSSOSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020
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 1321 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 Sequence 2, Application US/08443861

Patent No. 5851999

GENERAL INFORMATION, Axel

APPLICANT: Risau, Werner

APPLICANT: Millauer, Birgit

APPLICANT: Gazit, Alex

TITLE OF INVENTION: Flk-1 Is A Receptor For Vasci, TITLE OF INVENTION: Endothelial Growth Factor

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 the Americas
 ADDRESSEE: Pennie & Edm
STREET: 1155 Avenue of
 CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
 US-08-443-861-2
 199
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 YRSPFIASVSDQHGVVXITENKNKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWD 180
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 61 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 120
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 99.6%; Score 7070; DB 1; Length 1356; 99.6%; Pred. No. 0;
 4; Indels
 COUNTKX: COUNTKX: COUNTKX: COUNTKX: COUNTKX: COUNTKX: COUNTKX: COUNTKX: COUNTKY: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PALENT Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/930,548A FILING DATE: 23-NOV-1992

ATTORNEY/AGENT INFORMATION: A35 ATTORNEY/AGENT INFORMATION: NAME: GOACHO, Alan M. REGISTRATION NUMBER: 31,298-01

TELEPHONE: 201-831-3244

TELEPHONE: 201-831-324

TELEPAX: 201-831-324

TELEPAX: 201-831-324

TELEPAX: 201-831-326

INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:

LENGTH: 1356 amino acids

"WUED: COUNTY
 1; Mismatches
One Cyanamid Plaza
 Best Local Similarity 99.6
Matches 1351; Conservative
 MOLECULE TYPE: protein
 New Jersey
 Wayne
 STATE: Ne
 US-07-930-548A-8
 121
 181
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 421
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 Query Match
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1077 DRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRWRAPDYTTPEMYQT 1136
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 NRNLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFF
 APPLICANT: Ullrich, Axel
APPLICANT: Risau, Werner
APPLICANT: Risau, Werner
APPLICANT: Gail, Aviv
APPLICANT: Gail, Aviv
APPLICANT: Levitzki, Alex
TITLE OF INVENTION: Flk-1 IS A Receptor For Vascular
TITLE OF INVENTION: Endothelial Growth Factor
AUWBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmods
 1317 YSSDEAGLLKWVDAAVHA------DSGTTL 1340
 1319 YSSERAELLKLIEIGVQTGSTAQILQPDSGTTL 1351
 of the Americas
 ; Sequence 2, Application US/08193829B; Patent No. 6177401
 Avenue
 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FO
 GENERAL INFORMATION:
 STREET: 1155
 US-08-193-829B-2
 717
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 61 WIMPNAQRDSEERVLVTECGGGDSIFCKTLTIPRVVGNDTGAYKCSYRDVDIASTVYVYV 120
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 Gaps
 Length 1367;
 15;
 86.1%; Score 6106.5; DB 1; Length
85.8%; Pred. No. 0;
ive 71; Mismatches 106; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/443,861
FILING DATE: 22-MAY-1995
 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193,829
FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 766
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
 LENGTH: 1367 amino acids
 (212)869-9741
 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Conservative
 , MOLECULE TYPE: protein US-08-443-861-2
 amino acid
 Similarity
 Query Match
Best Local Simi
Matches 1161;
 TOPOLOGY:
 TELEFAX:
 61
 179
 181
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 241
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777 WILLVIVLRTVKRANEGELKTGYLSIVMDPDELPLDERCERLPYDASKWEFPRDRLKLGK
 LASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIF
 LASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIF
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 PLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNV
 VNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGKDYVGAIPVD
 1079 DRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQT
 DRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQT
 MLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSP
 1137 MLDCWHEDPNQRPSFSELVEHLGNLLQANAQQDGKDYIVLPMSETLSMEEDSGLSLPTSP
 VSCMEEBEVCDPKFHYDNTAGISOYLONSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQT
 1197 VSCMEEEEVCOPKFHYDNTAGISHYLQNSKRKSRPVSVKTFEDIPLEEPEVKVI PDDSQT
 1257 DSGMVLASEBLKTLEDRNKLSPSFGGMMPSKSRESVASEGSNQTSGYQSGYHSDDTDTTV
 1259 DSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTV
 TITLE OF INVENTION: F1k-1 IS A Receptor For Vascular Endothelial Growth Factor
 ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 1317 YSSDEAGLLKMVDAAVHA------DSGTTL 1340
 1319 YSSEBAELLKLIEIGVOTGSTAQILQPDSGTTL 1351
 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
 Sequence 2, Application US/09766678 Patent No. 6872699 GENERAL INFORMATION:
 Risau, Werner
Millauer, Birgit
Gazit, Aviv
Levitzki, Alex
 APPLICANT: Ullrich, Axel
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
 STATE: New York COUNTRY: U.S.A.
 CITY: New York
 US-09-766-678-2
 657
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 WLWPNNQSGSEQRVEVTEC--SDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYV 118
 238
 GEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVT 298
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 RSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYP 358
 PPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVY 418
 538
 536
 VPPQIGEKSLISPVDSYQYGTTQTLTCTVYALPPPHHIHWYWQLEEECANEPSQAVSVTN 478
 659 LTVLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKONETLVEDSGIVLKDG 718
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 QDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRIS
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 599 PTPVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQ
 MESKVILLAVALWICVETRAASVGLPSVSLDLPRISIOKDILTIKANTTLQITCRGQRDLD
 1 MESKALLAVALWFCVETRAASVGLTGDFLHPPKLSTQKDILTILANTTLQITCRGQRDLD
 Gaps
 15;
 Length 1367;
 106; Indels
 DB 2;
 #1.25
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
 71; Mismatches
 Score 6106.5;
Pred. No. 0;
 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,829B
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZI, DAULA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-060
TELECHONE: (212)790-9090
 86.1%;
85.8%;
 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 LENGTH: 1367 amino acids
 Matches 1161; Conservative
) MOLECULE TYPE: protein US-08-193-829B-2
 TYPE: amino acid
 Query Match
Best Local Similarity
 241
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LKRRLDSITSSOSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEF 1018
 LASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIF 1078
 1077 DRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQT 1136
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 PLGRGAFGQVIEADAFGIDKTATCKTVAVKMLKBGATHSEHRALMSELKILIHIGHHLNV
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 WLLLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGK
 DRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQT
 VSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQT
 DSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTV
 Sequence 4, Application US/07813593
Fatent No. 5185438
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSE: IMCLONE SYSTEMS INCORPORATED
STREET: 180 VARICK STREET
 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
 1317 YSSDEAGLLKMVDAAVHA------DSGTTL 1340
 YSSERAELLKLIEIGVQTGSTAQILQPDSGTTL 1351
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/813,593
FILING DATE: 19920415
CLASSIFICATION: 435
 Floppy disk
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 CITY: NEW YORK STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10014
 US-07-813-593-4
 837
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 GERVISFHVIRGPEITVOPAAQPTEQESVSLLCTADRNTFENLTWYKLGSQATSVHMGES 596
 118
 238
 476
 536
 GERVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGEL 598
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 VPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTN 478
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 QDYRSPF1ASVSDQHGVVY1TENKNKTVV1PCLGSISNLNVSLCARYPEKRFVPDGNRIS
 WDSKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVGYRIYDVVLSPSHGIELSV
 PYPCEEWRSVEDFQGGNKIEVNKNOPALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGR
 Gaps
 15;
 Length 1367;
 86.1%; Score 6106.5; DB 2; Length
85.8%; Pred. No. 0;
iive 71; Mismatches 106; Indels
 APPLICATION NUMBER: 08/193,829
FILING DATE: 09-FEB-1994
ATTORNEY/AGENT INFORMATION:
NEGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-060
 APPLICATION NUMBER: US/09/766,678
 2
 ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-766-678-2
 FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
 FELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
 LENGTH: 1367 amino acide
 CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 2:
 PRIOR APPLICATION DATA:
 Query Match
Best Local Similarity 85.8°
Matches 1161; Conservative
 479.
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897 VNLLGACTKPGGPLMVIVEFSKFGNLSTYLRGKRNEFVPYKSKGARFRQGKDYVGELSVD 956
 1137 MLDCWHEDPNORPSFSELVEHLGAILLOANAQODGKDYIVLPMSETLSMEEDSGLSLPTSP
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 957 LKRRLDSITSSQSSASGGFVEEKSLSDVEEERASEELYKDFLTLEHLICYSFQVAKGMEF
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 1017 LASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKAMAPETIF
 DRVYTIQSDVWSFGVLLWEIPSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQT
 1077 DRVYIIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRWRAPDYITPEMYQT
 MLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSP
 199 VSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQT
 1259 DSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTV
 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lemischka, Ihor R.

TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS

CORRESPONDENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Inclone Systems Incorporated
STREET: 180 Varick Street

CITY: New York

COUNTRY: New York

COUNTRY: U.S.A.
 PatentIn Release #1.0, Version #1.25
 1319 YSSEEAELLKLIEIGVQTGSTAQILQPDSGTTL 1351
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,451
FILING DATE: 19921119
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 6, Application US/07977451
Patent No. 5270458
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 FILING DATE: 19
CLASSIFICATION:
 657
 179
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 WLWPINNQSGSEQRVEVTEC - SDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYV 118
 QDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRIS 178
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 RSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYP 358
 421 VPPQIGEKALISPMDSYQYGTMQTLTCTVYANPPLHHIQWYWQLEEACSYRPGQ----TS 476
 536
 VPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTN 478
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 1 MESKGLLAVALWFCVETRAASVGLPGDFLHPPKLSTQKDILTILANTLLQITCRGQRDLD
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 WDSKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSV
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 Gaps
 Length 1367;
 15;
 85.9%; Score 6097.5; DB 1; Length
85.7%; Pred. No. 0;
tive 72; Mismatches 106; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-UNN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Peit, Irving N.
REGISTATION NUMBER: 28,601
REGISTATION NUMBER: 28,601
REGISTATION NUMBER: 28,601
REGISTATION NUMBER: 28,601
REGISTATION NUMBER: 28,601
 REFERENCE/DOCKET NUMBER: LEM-3-PPP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
 LENGTH: 1367 amino acids
 TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Best Local Similarity 85.7
Matches 1160; Conservative
 ; MOLECULE TYPE: protein US-07-813-593-4
 TYPE: AMINO ACID
 61
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 Query Match
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 1257 DSGWVLASEELKTLEDRNKLSPSFGGMMPSKSRESVASEGSNQTSGYQSGYGSGDTDTTV 1316
 176
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 598
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 LASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIF
 DSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTV
 VPPQ1GEKSL1SPVDSYQYGTTQTLTCTVYA1PPPHH1HWYWQLEEECANEPSQAVSVTN
 PYPCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGR
 GERVISFHVTRGPEITLOPDMOPTEOESVSLWCTADRSTFENLTWYKLGPOPLPIHVGEL
 PTPVCKNLDTLWKLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQ
 LIVLERVAPILIGNLENQTISIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDG
 NRNLTIRRVRKEDEGLYTCOACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFF
 WILLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGK
 PLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNV
 DRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQT
 MLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSP
 VSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQT
 TOTIPOTENT HEMATOPOIETIC STEM CELL
 YSSDEAGLLKMVDAAVHA------DSGTTL 1340
 YSSEEAELLKLIEIGVQTGSTAQILQPDSGTTL 1351
 Sequence 4, Application US/07946507; Patent No. 5283354; GENERAL INFORMATION:
 Ihor R
 Lemischka,
 APPLICANT: Lemischk
TITLE OF INVENTION:
 US-07-946-507-4
 479
 477
 539
 537
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 657
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 WLWPNNQSGSEORVEVTEC -- SDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYV 118
 RSDQCLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYP 358
 PPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVY 418
 361 APDIKWYRNGRPIESNYTMIVGDELTIMEVTERDAGNYTVILTNPISMEKQSHMVSLVVN 420
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 GEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVT
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 WDSKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSV
 Gaps
 Length 1367;
 15;
 Indels
 DB 1;
 106;
 85.9%; Score 6097.5;
llarity 85.7%; Pred. No. 0;
Conservative 72; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
 APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
 APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/728,913
 PRIOR APPLICATION NUMBER: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-ARR-1991
ATTORNEY/AGENT INFORMATION:
 LEM-3-7P
 US UNASSIGNED
 US 07/813,593
 28,601
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
 FILING DATE: 24-DEC-1991 PRIOR APPLICATION DATA:
 12-NOV-1992
 26-JUN-1992
 REFERENCE/DOCKET NUMBER:
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1367 amino acti
 NAME: Feit, Irving N. REGISTRATION NUMBER:
 212-645-2054
 APPLICATION NUMBER: UFILING DATE: 12-NOV-1PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
 , MOLECULE TYPE: protein US-07-977-451-6
APPLICATION DATA:
 LENGTH: 1367 amir
TYPE: AMINO ACID
 Query Match
Best Local Similarity
Matches 1160; Conserv
 FILING DATE:
 TOPOLOGY:
 121
 359
 61
 61
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85.7%; Pred. No. 0;
ive 72; Mismatches 106; Indels
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CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/07/946,507
FILING DATE: 19920917
CLASSIFICATION: 536
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 1
CORRESPONDENCE ADDRESS: INCLONE SYSTEMS INCORPORATED STREET: 180 VARICK STREET
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION NUMBER: US/07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,913
APPLICATION NUMBER: US/07/728,913
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APPLICATION NUMBER: US/07/728,913
FILING DATE: 02-APR-1991
ATTORNEY AGENT INFORMATION:
NAME: US/07/679,666
 NAME: Feit, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-PPP
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
 TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 1367 amino acids
TYPE: AMINO ACID
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Best Local Similarity 85.73
Matches 1160; Conservative
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CITY: NEW YORK
STRIE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
 ; MOLECULE TYPE: protein US-07-946-507-4
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 APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
TITLE OF INVENTION: RECEPTORS AND THEIR LIGANDS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
 85.9%; Score 6097.5; DB 1;
llarity 85.7%; Pred. No. 0;
Conservative 72; Mismatches 106;
 PatentIn Release #1.0, Version #1.25
 E: ImClone Systems Incorporated 180 Varick Street
 US PCT/US92/05401
 US PCT/US92/02750
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-UN-1992
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FILING DATE: 26-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/0275
FILING DATE: 02-APR-1992
PRIOR APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
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FILING DATE: 15-NOV-1991
PRIOR APPLICATION NUMBER: US 07/728,913
FILING DATE: 15-NOV-1991
PRIOR APPLICATION NUMBER: US 07/728,913
FILING DATE: 15-NOV-1991
PRIOR APPLICATION NUMBER: US 07/728,913
FILING DATE: 15-NOV-1991
PRIOR APPLICATION NUMBER: US 07/728,913
FILING DATE: 24-DADA-1992
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,517
FILING DATE: 31-0CT-1994
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
 FILING DATE: 19-NOV-1992
 FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
 REPERENCE/DOCKET NUMBER:
 1367 amino acids
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 NAME: Feit, Irving N.
REGISTRATION NUMBER: 2
 MOLECULE TYPE: protein
 New York
: U.S.A.
 Similarity
 FILING DATE: 31 CLASSIFICATION:
 GENERAL INFORMATION
 CITY: New York
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 COUNTRY:
 US-08-252-517-6
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	AMT: Tebben, Anaran  AMT: Tebben, Andrew OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE EBFRERNCE: 19963YDB  TY APPLICATION NUMBER: US/10/022,939  TY FILING DATE: 2000-1.14  APPLICATION NUMBER: 09/483,539  FILING DATE: 1998-06-17  PILING DATE: 1998-06-17  APPLICATION NUMBER: 60/050,962  FILING DATE: 1998-06-18  APPLICATION NUMBER: 60/050,962  FILING DATE: 1998-06-18  TO FSG 1D NOS: 8  NO FSG 1D NOS: 8  THE THAT THE TEST TEST TEST TEST TEST TEST TEST	4 ,	MESKVILAVALMLCVETRAASVQLPSVSLDLPRLSIQKDILIIKANTTLQIT 
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 Length 1356;
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 CENERGAL INFORMATION:
APPLICANT: Kendall, Richard L.
APPLICANT: Thomas, Kenneth A.
APPLICANT: Thomas, Kenneth A.
APPLICANT: Thomas, Kenneth A.
APPLICANT: Tebben, Andrew
TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KJ
FILE REFERENCE: 1996-873DC
CURRENT APPLICATION NUMBER: US/10/100,405A
CURRENT APPLICATION NUMBER: U0/022,939
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2000-01-14
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1356
 100.0%; Score 7095; llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
Sequence 2, Application US/10100405A; Publication No. US20030055239A1; GENERAL INFORMATION:
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 Query Match
Best Local Simil
Matches 1356; C
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0; Mismatches
 100.0%;
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Best Local Similarity 100.
Matches 1356; Conservative
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; ORGANISM: Homo
US-10-327-414-6
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'Sequence 6, Application US/10327414

's Sequence 6, Application US/10327414

'publication No. US2030158083A1

'GENERAL INFORMATION:
'APPLICANT: The Procter & Gamble Company
'APPLICANT: The Procter & Gamble Company
'APPLICANT: Peters, Kevin G

'TITLE OF INVENTION: A Method of Effecting angiogenesis by Modulating the Funct
'TITLE OF INVENTION: B. Method of Effecting angiogenesis by Modulating the Funct
'TITLE OF INVENTION: Endothelia Phosphatase
'TITLE OF INVENTION: B. Method of Effecting angiogenesis by Modulating the Funct
'TITLE OF INVENTION: Endothelia Phosphatase
'TITLE OF INVENTION NUMBER: US/10/327,414
'CURRENT APPLICATION NUMBER: US 60/355,125
'PRIOR PRILING DATE: 2002-02-08
'NUMBER OF SEQ ID NOS: 9
'SOFTWARE: Patentin version 3.1
'SEQ ID NO 6
'LENGTH: 1356
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 US-10-165-193A-11

Sequence 11, Application US/10165193A

Publication No. US20030207391A1

GENERAL INFORMATION:
APPLICANT: HELEN PAPPA

TITLE OF INVENTION: BINDING PROTEIN
FILE REFRENCE: 1396-1-00
CURRENT APPLICATION NUMBER: US/10/165,193A

CURRENT APPLICATION NUMBER: PCT/GE00/04693

PRIOR PILING DATE: 2000-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 16

SOFTWARE: SEQWIN99, version 1.02

LENGTH: 1356
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100.0%; Score 7095;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches
 TYPE: PRT
ORGANISM: Homo sapiens
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 Sequence 66, Application US/10394322A

Publication No. US2003023391A1

GRERAL INFORMATION

APPLICANT: STESCOLY, JOHN C.

TITLE OF INVENTION: IDENTIFICATION OF KINASE INH

FILE REFERENCE: 39750-0006 US

CURRENT APPLICATION NUMBER: US/10/394,322A

CURRENT APPLICATION NUMBER: US 60/366,892

PRIOR RPLICATION NUMBER: US 60/366,892

PRIOR FILING DATE: 2002-03-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 4.0

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Best Local Similarity 99.9%;
Matches 1355; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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 Sequence 2, Application US/10090183
Sequence 2, Application US/10090183
Publication No. US20030185802A1
GENERAL INFORMATION:
APPLICANT: Ralph A. Reisfeld
APPLICANT: Ralph A. Reisfeld
APPLICANT: Ralph A. Reisfeld
APPLICANT: Rong Xiang
TITLE OF INVENTION: DNA VACCINE ACAINST PROLIFERATING
TITLE OF INVENTION: ENDOTHELIAL CELLS AND METHODS OF USE THEREOF
FILE REFERENCE: TSRI-829.0
CURRENT PILING DATE: 2002-03-02
CURRENT PILING DATE: 2002-03-02
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
 ö
 99.9%; Score 7092; DB 4; Length 1356; 99.9%; Pred. No. 0; ive 1; Mismatches 0; Indels 0
 Query Match 99.9
Best Local Similarity 99.9
Matches 1355; Conservative
 ; TYPE: PRT
; ORGANISM: human
US-10-090-183-2
 LENGTH: 1356
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 SEQ ID NO 2
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RESULT 8
US-10-783-528-61
Sequence 61, Application US/10783528
Fublication No. US20040219579A1
Fublication No. US20040219579A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kuzet
APPLICANT: Gish, Kuzet
APPLICANT: INVENTION: METHOR OF DIAGNOSIS OF CANCER, COMPOSITIONS AND FILE OF INVENTIONS METHORS OF DIAGNOSIS OF CANCER, CURRENT APPLICATION NUMBER: US/10/783,528
CURRENT APPLICATION NUMBER: US/10/783,528
CURRENT APPLICATION NOWER: 116
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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 Length 1356;
 IndelB
 DB 5;
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 Score 7092; DE Pred. No. 0; 1; Mismatches
 90.06
 Query Match
Best Local Similarity 99.9
Matches 1355; Conservative
 ; ORGANISM: Homo Sapiens
US-10-783-528-61
 LENGTH: 1356
TYPE: PRT
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 5; Length 1356;
 Indels
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 1; Mismatches
 Query Match
99.9%; Score 7092;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1355; Conservative 1; Mismatche
SOFTWARE: PatentIn version 3.1 SEQ ID NO 115 LENGTH: 1356 TYPE: PRT ORGANISM: Homo sapiens
 US-10-872-198-115
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 APPLICANT: Andreas SCHEIDIG
APPLICANT: Andreas SCHEIDIG
APPLICANT: Andreas SCHEIDIG
APPLICANT: Andreas SCHEIDIG
APPLICANT: Christian VOETSMEIER
APPLICANT: Christian VOETSMEIER
APPLICANT: Ulrich Kettling
TILLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
FILE REPERENCE: 04156.0002U4
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR PILING DATE: 2003-11-21
PRIOR PILING DATE: 2003-11-11
PRIOR PILING DATE: 2003-11-11
PRIOR PILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR PILING DATE: 2003-11-10
PRIOR PILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR APPLICATION NUMBER: EP 03025861
PRIOR APPLICATION NUMBER: EP 03025861
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-16-18
 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 US-10-872-198-115; Sequence 115, Application US/10872198; Publication No. US20050002897A1; GENERAL INFORMATION:
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Sequence 1469, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

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 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 VYTIQSDVWSPGVLLWEI FSLGASPY PGVKIDBEFCRRLKEGTRWRAPDYTTPEMYQTML
 GMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE
 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLERPEVKVIPDDNQTDS
 WLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD
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 Length 1356;
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQ:
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 DB
 99.9%; Score 7092; I 99.9%; Pred. No. 0; ive 1; Mismatches
 Conservative
 ; ORGANISM: Homo sapiens
US-10-741-600-1469
 Query Match
Best Local Similarity
Matches 1355; Conserv
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 TYPE: PRT
ORGANISM:
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 1261 GMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS
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 OCULAR
 JULY SEGUENCE 10, APPLICATION US/10926806

Publication No. US20050096257A1

FRERRAL INFORMATION:

APPLICANT: GALIAS, PERRY

APPLICANT: CALIAS, PERRY

APPLICANT: ANAMIS, ANTHONY P.

ITLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCUL.

ITLE OF INVENTION: COMBINATION THERAPY FOR THE TREATMENT OF OCUL.

ITLE OF INVENTION: NEWDASCULAR DISORDERS

FILE REFERENCE: 112089.184 EYE-013

CURRENT FILING DATE: 2004-08-26

FRIOR APPLICATION NUMBER: 60/556,837

FRIOR APPLICATION NUMBER: 60/556,837

FRIOR PILING DATE: 2003-08-27

FRIOR PILING DATE: 2003-08-27

FRIOR PILING DATE: 2003-08-27

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FRIOR FILING DATE: 2003-08-27
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 Score 7092; DB Pred. No. 0;
 Query Match
Best Local Similarity 99.9%;
Matches 1355; Conservative
 RESULT 12
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 Sequence 1471, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION.
TITLE OF INVENTION: MICHAEL Et al.
TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FREESEQ for Windows Version 4.0
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 420
 120
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 PCEEWRS VED F QGGNKI EVNKNOFAL I EGKNKTVSTLVI QAANVSAL YKCEAVNKVGRGE
 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT
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 DB 5; Length 1356;
 0; Indels
 Score 7092; D
Pred. No. 0;
1; Mismatches
 99.98;
 Query Match
Best Local Similarity 99.9°
Matches 1355, Conservative
 trype: PRT
CRGANISM: Homo sapiens
US-10-741-600-1471
 RESULT 11
US-10-741-600-1471
 LENGTH: 1356
 SEQ ID NO 1471
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	RESULT 13 US-10-824-982-2 ; Sequence 2, Application US/10824982 ; Sequence 2, Application No. US20050197492A1 ; GENERAL INFORMATION: ; APPLICANT: Inventors: Michele A. McTigue, Steven L. Bender, Allen Borchardt, Robert ; APPLICANT: Kania, Chris Pinko, John A. Wickersham ; TTILE OF INVENTION: Methods of Use Thereof ; TITLE OF INVENTION: Methods of Use Thereof ; FILE REFERENCE: PC19173A ; CURRENT APPLICATION NUMBER: US/10/824,982 ; CURRENT PILING DATE: 2004-04-15 ; NUMBER OF SEQ ID NOS: 11 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 2 ; LENGTH: 1356	TYPE: PRT ORGANISM: Homo sapiens 10-824-982-2  Ouery Match  10-824-982-2  Duery Match  11 Mismatches 0; Length 1356;  Best Local Similarity 99.9%; Pred. No. 0;  Best Local Similarity 99.9%; Pred. No. 0;  I MESKVLLAVALMICVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD	Db 121 YRSPFIASVSDQHGVVYITENKKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWD 180  Qy 181 SKKGFTIPSYMISYAGMVPCBAKINDESYQSIMYIVVVGYRIYDVULSPSHGIELSVGE 240  181 SKKGFTIPSYMISYAGMVPCBAKINDESYQSIMYIVVVGYRIYDVULSPSHGIELSVGE 240  Qy 241 KLVLACTARTELAVGIDPNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300  241 KLVLACTARTELAVGIDPNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300  Qy 301 DQGLYTCARTELAVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300  Qy 301 DQGLYTCAASSGLMTKRNSTFVRVHEKPFVAFGSGMESLVAATVGERVRIPAKYLGYPPP 360  Qy 361 DQGLYTCAASSGLMTKRNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360  Qy 361 BIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP 420  B BIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP 420	
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 Length 1356;
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 APPLICANT: VOUSMELEK, Currectan.
APPLICANT: COCO, Wayne Michael
APPLICANT: COCO, Wayne Michael
TITLE OF INVENTION: New Biological Entities And The
TITLE OF INVENTION: New Biological Entities And The
TITLE OF INVENTION: New Biological Entities And The
TITLE OF INVENTION: New Biological Entities And The
TITLE OF INVENTION: And Diagnostic Use Thereof
FILE REFERENCE: 04156.000205
CURRENT APPLICATION NUMBER: 10/812,198
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/524,960
PRIOR PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2003-11-25
PRIOR PRIOR APPLICATION NUMBER: EP 03025871
PRIOR FILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR PRIOR APPLICATION NUMBER: EP 03025851
PRIOR PRIOR OFFICE 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
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SROOFWARE: PACENTIN NUMBER: EP 03013819
NUMBER OF SEQ ID NOS: 191
SEQ ID NO 115
LENGTH: 1356
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99.9%; Score 7092; Dest Local Similarity
99.9%; Pred. No. 0;
Matches 1355; Conservative 1; Mismatches
 ; ORGANISM: Homo sapiens
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Sequence 115, Application US/11021951; Publication No. US20050175581A1; GENERAL INFORMATION:
APPLICANT: HAUPTS, UIT.
APPLICANT: KOLTERWANN, Andre
APPLICANT: SCHEIDIG, Andreas

RESULT 14 US-11-021-951-115

; TYPE: PRT ; ORGANISM: Human US-09-969-037-7	Query Match 99.9%; Score 7091, DB 3, Length 1356; Best Local Similarity 99.9%; Pred. No. 0, Matches 1354; Conservative 2; Mismatches 0; Indels 0, Gaps 0	QY 1 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD 60	nnosgseorvevtecsdglecktlipkvigndtgaykcpyretdlasviyvy 	121 YRSPFIASVSDQHGVVYITENKAKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNR 121 YRSPFIASVSDQHGVVYITENKAKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNR	181 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 2 181 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 2	241 KLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 3 [	301 DOGLYTCAASSGLMTKKNSTFYRVHEKFYAFGSGMEGLVEATVGERYRIPAKYLGYPPP 3 	361 BIKWYKNGIPLESNHTIKAGHULTIMEVSERDTGNYTYILTNFISKEKOSHVUSLUVYVP 4 	Qy 421 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEEECANEPSQAVSVTNPY 480	QY 481 PCEEWRSVEDFQGGNKIEVNKNQFALLEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE 540	Oy 541 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT 600	Qy 601 PVCKNLDTL#KLNATWFSNSTNDILIMELKNASLQDQGDYVCLAQDRRTKKRHCVVRQLT 660	OY 661 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPQIMWFKDNETLYEDSGIVLKDGNR 720	QY         721 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL 780           L	QY 781 LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL 840	Qy 841 GRGAFGQVIEADAFGIDKTATCRTVAVKMLKBGATHSEHRALMSELKILIHIGHHLNVVN 900	OY 901 LIGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFROGKDYVGAIPVDLK 960	Qy 961 RRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 102	
OY 601 PVCKNLDTLWKLNATMFSNSTNDILIMELKNASLODQGDYVCLAQDRKTKKRHCVVRQLT 660	661 VLERVAPTITGNLENGTEIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR	721 NLTIRRVRKEBEGLYTCOACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIANFFWL 78 721 NLTIRRVRKEBEGLYTCOACSVLGCAKVEAFFIIEGAQEKTNLEIIILVGTAVIANFFWL 78	781 LLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL 8	GRGAFGQVI EADAFGIDKTATCRTVAVKALKEGATHSEHRALMSELKILHIGHHLNVVN 90 	GAIPVDLK 9          GAIPVDLK 9	Qy         961 RRLDSITSSQSSASSGFVEEKSLSDVBEBERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020           Db         961 RRLDSITSSQSSASSGFVEEKSLSDVBEBEAPEDLYKDFLTLEHLICYSFQVAKGMEFLA 1020	Qy 1021 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPBTIFDR 1080	OY 1081 VYTIQSDVWSFGVLAWEIFSLGASPYFGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTWL 1140	OY         1141 DCWHGEPSQRPTPSELVEHLGNLLQANAQQDGKDYIVLEISETLSMEEDSGLSLPTSPVS 1200           Dh         1141 DCWHGEPSQDPPPSELVEHLGNLLQANAQQDGKDYIVLEISETLSMEEDSGLSLPTSPVS 1200	1201 CMEREFUCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS 120 1201 CMEREFUCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS 126 1201 CMEREFUCDPKFHYDNTAGISQYLQNSKRKSRPDSGYKFFFFIPIFREFUKVIPDDNQTDS 126 1201 CMEREFUCDPKFHYDNTAGISQYLQNSKRKSRPDSGYKFFFFIPIFREFUKVIPDDNQTDS 126	1261 GWLASBELKTLEDRIKKLSPSFGGWPSKSRESVASEGSNQTSGYOGYHSDDTDTTVYS 132 1261 GWLASBELKTLEDRITKLSPSFGGWPSKSRESVASEGSNQTSGYOGGYHSDDTDTTVYS 132 1261 GWLASBELKTLEDRITKLSPSFGAWPSKSRESVASEGSNOTSGYOGGYHSDDTDTTVYS 132	1321 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356 1321 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356 1321 SEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356	SULT 15	US-959-03-03-7; Sequence 7, Application US/09969037; Publication No. US20030022247A1; GENERAL INFORMATION:	<ul> <li>APPLICANT: KYOWA HAKKO KOGYO CO., LID.</li> <li>ITILE OF INVENTION: Substance which inhibits biding of information transfer molecule.</li> <li>ITILE OF INVENTION: for 11/5-tyrosine phosphorylated KDR/FIK-1 and usages of the sample RILE REFERENCE:</li> </ul>	; CURRENT APPLICATION NUMBER: US/09/969,037 ; CURRENT FILING DATE: 2001-10-03 ; PRIOR APPLICATION NUMBER: JP 2000-303694 ; PRIOR FILING DATE: 2000-10-03	FILOR APPLICATION NUMBER: US 60/263,512 FILOR FILING DATE 2001-01-24 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.1	SEQ 1D NO 7 LENGTH: 1356	

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## ALIGNMENTS

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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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Sequence 904, Application US/10995561 Publication No. US20050272054A1 GENERAL INFORMATION:
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Best Local Similarity 99.9
Matches 1355; Conservative
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; GENERAL INFORMATION:  APPLICANT: CARGILL, Michele et al.  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  TITLE OF INVENTION: DETECTION AND USES THEREOF  TITLE OF INVENTION: DETECTION AND USES THEREOF  FILE REFERENCE: CLOOIS59  CURRENT APPLICATION NUMBER: US/10/995,561  CURRENT FILING DATE: 2004-11-24  NUMBER OF SEQ ID NOS: 85702  SEQ ID NO 906  LENGTH: 1356  LENGTH: 1356  TYPE: PRT  ORGANISM: Homo sapiens  US-10-995-561-906	Query Match 99.9%; Score 7092; DB 6; Length 1356; Best Local Similarity 99.9%; Pred. No. 0; Matches 1355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Qy 1 MESKVLLAVALMLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD 60	Qy	QY         121 YRSPFIASVSDQHGVVYITENKAYKTVVIPCLGSISNLAVSLCARYPEKRFVPDGNRISWD 180	Qy 181 SKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGE 240	QY 241 KLVINCTARTEINVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300 241 KLVLNCTARTEINVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRS 300	Qy 301 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360 10 DQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360	QY         361 BIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP 420           DD         361 BIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTNPISKEKQSHVVSLVVYVP 420	QY         421 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEECANEPSQAVSVTNPY 480           DD         421 PQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQLEECANEPSQAVSVTNPY 480	QY 481 PCEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGE 540	OY 541 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT 600	QY         601 PVCKNLDTL#KLNATMFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLT         660	Qy 661 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR 720	QY 721 NLTIRRVRKEDEGLYTCQACSVLGCAKVBAFFIIEGAQEKTNLEIIILVGTAVIAMFFWL 780	
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 LIVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPL
 VYTIOSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTML
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 WLWPNNQSGSEORVEVTECSDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQD 120
 121 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD 180
 60
 9
 Sequence 905, Application US/10995561
| Publication No. US20050272054A1
| GENERAL INFORMATION: Michele et al. | APPLICANT: CARGILL, Michele et al. | APPLICANT: CARGILL, MICHELE et al. | TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: DETECTION AND USES THERROF | TITLE OF INVENTION: DETECTION AND USES THERROF | FILE REFRENCE: CLO01559 | CURRENT PEDILGON AND USES THERROF | CURRENT PEDILG DATE: 2004-11-24 | NUMBER OF SEQ ID NOS: 85702 | SEQ ID NOS: 85702 | SEQ ID NO 905 | SEQ ID NO 905 | LENGTH: 1306 |
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 VYTIOSDVWSFGVLLWEI FSLGASPYPGVXIDEEFCRRLKEGTRMRAPDYTTPEMYOTML
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 RRLDSITSSQSSASSGFVEEKSLSDVEEERAPEDLYKDFLTLEHLICYSFQVAKGMEFLA
 SRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDR
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 Gaps
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 Length 1306;
 1; Indels
 SERAELLKULEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 DB 6;
 Query. Match 95.9%; Score 6806; D
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1303; Conservative 2; Mismatches
 1 TYPE: PRT
7 ORGANISM: Homo sapiens
US-10-995-561-905
 RESULT 3
US-10-995-561-905
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APPLICANT: Davis-Smyth, Terri L.
APPLICANT: Chen, Helen H.
APPLICANT: Chen, Helen H.
APPLICANT: Presta, Leonard
APPLICANT: Presta, Leonard
APPLICANT: Perrara, Napoleone
TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
 661 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMMPKDNETLVEDSGIVLKDGNR 720
 541 RVISFHVTRGPEITLQPDMQPTEQESVSLWCTADRSTFENLTWYKLGPQPLPIHVGELPT 600
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 VLERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNR
 ö
 721 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLE 764
 NLTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLE 764
 Indels
 COMPUTER: FIDERY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/043,693
FILING DATE: 26-Jan-2005
CLASSIFICATION:
 ö
 Score 4017; DB 7;
Pred. No. 1.5e-247;
 NAME: Richard F. Trecartin
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC
TELECOMMUNICATION:
TELEPHONE: (415) 781-1989
 1; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/105,901
FILING DATE: 20-Mar-2002
APPLICATION NUMBER: 09/348,886
FILING DATE: 01-JUL-1999
APPLICATION NUMBER: US 08/643,839
FILING DATE: 07-MAX-1996
ATTORNEY/AGENT INFORMATION:
 Sequence 2, Application US/11043693
Publication No. US20050281831A1
GENERAL INFORMATION:
 56.6%;
 TELERX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
 STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 SEQUENCE CHARACTERISTICS:
LENGTH: 767 amino acids
 (415) 398-3249
 763; Conservative
 MOLECULE TYPE: protein
 Query Match
Best Local Similarity
Matches 763; Conserva
 STRANDEDNESS:
 US-11-043-693-2
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1151 CMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDS 1210
 GWVLASEELKTLEDRTKLSPSFGGWVPSKSRESVASEGSNQTSGYQSGYHSDDTDTTVYS 1320
 Sequence 4, Application US/11075047A
Publication No US20060030000A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
FILE REFRENCE: 289567/39700A
CURRENT APPLICATION NUMBER: US/11/075,047A
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US/60/550,907
PRIOR FILING DATE: 2004-03-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.2
LENGTH: 764
 121 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD 180
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 YRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWD 180
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 DOGLYTCAASSGLMTKKNSTFVRVHEKPPVAFGSGMESLVEATVGERVRIPAKYLGYPPP 360
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 Gaps
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 Length 764;
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 Score 4020; DB 7; I
Pred. No. 9.9e-248;
 56.7%; Sco...
100.0%; Pred. No....
0; Mismatches
 Local Similarity 100.
1es 764; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 US-11-075-047A-4
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 122 RSPFIASVSDQHGVVYITENKOKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWDS
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 602 VCKNLDTLWKLNATWFSNSTNDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLTV
 LERVAPTITGNLENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRN
 CEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGER
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 Length 764;
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 764
 Sequence 28, Application US/11104111
; Publication No. US20060024289A1
; Fublication No. US20060024289A1
; GENERAL INFORMATION:
; APPLICANT: Waugh Ruggles, Sandra
; APPLICANT: Waugh Ruggles, Sandra
; APPLICANT: Wguyen, Jack
; TITLE OF INVENTION: CLEAVAGE OF VEGF AND VEGF RECEPTOR 1;
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: 25840-503
; CURRENT APPLICATION NUMBER: US/11/104,111
; CURRENT FILING DATE: 2005-04-12
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 Score 4012; DB 7;
Pred. No. 3.2e-247;
1; Mismatches 0;
 . 56.5%;
 Best Local Similarity 99.9
Matches 762; Conservative
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 ; TYPE: PRT
; ORGANISM: Homo
US-11-104-110-8
 RESULT 7
US-11-104-111-28
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 APPLICANT: Ruggles, Sandra
APPLICANT: Ruggles, Sandra
APPLICANT: Ruggles, Sandra
APPLICANT: Ruggles, Sandra
APPLICANT: Nguyen, Jack
TITLE OF INVENTION: CLEAVAGE OF VEGF AND VEGF RECEPTOR BY WILDTYPE AND MUTANT MT-SP1
FILE REPERENCE: 25840-502
CURRENT FILING DATE: 2005-04-12
PRIOR PILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 60/561,720
PRIOR PILING DATE: 2004-04-12
PRIOR PILING DATE: 2004-07,977
PRIOR PILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR PILING DATE: 2002-10-02
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 Sequence 8, Application US/11104110; Publication No. US20060002916A1; GENERAL INFORMATION:
 LENGTH: 764
 121
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 181
 241
 241
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 181
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 361
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 KKGFTIPSYMISYAGMVFCBAKINDESYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGEK 241
 241
 QGLYICAASSGLMIKKNSTFVRVHEKPFVAFGSGMESLVEATVGERVRIPAKYLGYPPPE 361
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 Gaps
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 56.5%; Score 4012; DB 7; Length 764; 99.9%; Pred. No. 3.2e-247; ive 1; Mismatches 0; Indels
 764
 LTIRRVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQEKTNLE
 PRIOR APPLICATION NUMBER: 60/561,671
PRIOR FILING DATE: 2004-04-12
PRIOR PRICATION NUMBER: 10/677,977
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 28
 Query Match 56.5
Best Local Similarity 99.9
Matches 762; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 US-11-104-111-28
 302
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RESULT 8 US-11-104-110-9

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; Sequence 9, Application US/11104110
; Publication No. US20060002916A1
; GENERAL INFORMATION:
; APPLICANT: Ruggles, Sandra
; APPLICANT: Ruggles, Sandra
; APPLICANT: Ruggles, Candra
; TITLE OF INVENTION: CLEAVAGE OF VEGF AND VEGF RECEPTOR BY WILDTYPE AND MUTANT MT-SP1
; FILE REFERENCE: 25840-502
; CURRENT APPLICATION NUMBER: US/11/104,110
; CURRENT FILING DATE: 2004-04-12
; PRIOR APPLICATION NUMBER: 10/671,977
; PRIOR APPLICATION NUMBER: 10/677,977
; PRIOR APPLICATION NUMBER: 06/415,388
; PRIOR APPLICATION NUMBER: 06/415,388
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 592
 1004
 1064
 1124
 1304
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 1125 MRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETL 1184
 1185 SMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPL 1244
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 180
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 300
 420
 480
 540
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 884
 944
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 121 ELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGAR
 181 FRQGKDYVGAIPVDLKRRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEH
 241 LICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGD
 301 ARLPLKAWAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTR
 361 MRAPDYTTPEMYQTWLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETL
 481 BEPEVKVIPDDNQTDSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSG
 765 IIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDA
 1 IIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDA
 SKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKWLKEGATHSEHRALMS
 61 SKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMS
 ELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGAR
 945 FRQGKDYVGAIPVDLKRRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEH
 1005 LICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGD
 1065 ARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTR
 421 SMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPL
 EEPEVKVIPDDNQTDSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSG
 YQSGYHSDDTDTTVYSSERAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 592
 ö
 YQSGYHSDDTDTTVYSSEEAELLKLISIGVQTGSTAQILQPDSGTTLSSPPV
 Query Match
43.3%; Score 3075; DB 7; Length 592;
Best Local Similarity 100.0%; Pred. No. 7.9e-188;
Matches 592; Conservative 0; Mismatches 0; Indels
 US-11-104-111-29; Sequence 29, Application US/11104111
; Publication No. US2060024289A1
; GENERAL INFORMATION:
) ORGANISM: Homo sapiens
US-11-104-110-9
 825
 885
 1245
 1305
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us-10-633-742-6.rapbn

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APPLICANT: Ferral
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: GROWTH FACTOR ALL
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dorsey & Whitney LLP
"""RET: Four Embarcadero Center, Suite 3400
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-63291-3/RFT/NBC
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/105,901
FILING DATE: 20-Mar-2002
APPLICATION NUMBER: 09/348,886
FILING DATE: 01-JUL-1999
APPLICATION NUMBER: US 08/643,839
FILING DATE: 07-MAY-1996
ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: US/11/043,693
FILING DATE: 26-Jan-2005
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
 NAME: Richard F. Trecartin
 TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 34:
 FELECOMMUNICATION INFORMATION
 TELEPHONE: (415) 781-1989
 SEQUENCE CHARACTERISTICS:
LENGTH: 1368 amino acids
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 TOPOLOGY: unknown MOLECULE TYPE: protein
 TYPE: amino acid
STRANDEDNESS: unl
 94111-4187
 CLASSIFICATION:
 FILING DATE:
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APPLICANT: Waugh Ruggles, Sandra
APPLICANT: Nguyen, Jack
TITLE OF INVENTION: CLEAVAGE OF VEGF AND VEGF RECEPTOR BY WILD-TYPE AND MUTANT
TITLE OF INVENTION: PROTEBASES
 FRQGKDYVGAIPVDLKRRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEH 1004
 LICYSPQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGD 1064
 1065 ARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTR 1124
 MRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYIVLPISETL 1184
 SMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPL 1244
 EEPEVKVIPDDNQTDSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSG 1304
 61 SKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMS 120
 241 LICYSFQVAKGMEFLASRKCIHRDLAARNILLISEKNVVKICDFGLARDIYKDPDYVRKGD 300
 421 SMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDIPL 480
 ELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGAR 944
 MRAPDYTTPEMYOTMLDCWHGEPSORPTFSELVEHLGNLLOANAOODGKDYIVLPISETL 420
 1 IIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLSIVWDPDELPLDEHCERLPYDA 60
 481 BEPEVKVIPDDNQTDSGMVLASEELKTLEDRIKLSPSFGGMVPSKSRESVASEGSNQTSG
 SKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKWLKEGATHSEHRALMS
 ELKILIHIGHHLAVVNLLGACTKPGGPLAVIVEFCKFGNLSTYLRSKRNEFVPYKTKGAR
 181 FROGKDYVGAIPVDLKRRLDSITSSOSSASSGFVERKSLSDVEEEEAPEDLYKDFLTLEH
 301 ARLPLKWAAPETIFDRVYTIQSDVWSFGVLLWBIFSLGASPYPGVKIDEEFCRRLKEGTR
 765 IIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDA
 Gaps
 YOSGYHSDDTDTTVYSSEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 1356
 541 YQSGYHSDDTDTTVYSSEEAELLKLIEIGVQTGSTAQILQPDSGTTLSSPPV 592
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 Length 592;
 0; Indels
 Score 3075; DB // No. 7.9e-188;
 43.3%; Sco...
100.0%; Pred. No. ...
0; Mismatches
 FILE REFERENCE: 25840-503
CURRENT APPLICATION NUMBER: US/11/104,111
CURRENT FILING DATE: 2005-04-12
 CURRENT FILING DATE: 2005-04-12
PRIOR APPLICATION NUMBER: 60/561,671
PRIOR FILING DATE: 2004-04-12.
PRIOR APPLICATION NUMBER: 10/677,977
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER: 60/415,388
SOFTWARE: PROS: 43
 US-11-043-693-34
; Sequence 34, Application US/11043693
; Publication No. US20050281831A1
; GENERAL INFORMATION:
APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
 Query Match 43.3
Best Local Similarity 100.
Matches 592; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-104-111-29
 SEO ID NO 29
 945
 1005
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 RESULT 10
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NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
PRODUCTION
 118 KARIEGTTAASIYIFISDTGRPFVEMYSEIPEIIHMTEGRE--LVIPCRVTSPAITVTL- 174
 60 DWLWPNNQSG-----SEQRVEVTECSDGL----FCKTLTIPKVIGNDTGAYKCFYR-- 106
 107 ----ETDLASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLC 162
 163 ARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYR 222
 223 IYDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHOHKKLVNRDLKTQSG 282
 283 SEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEA 342
 1 MORGAALCIRIWICIGILDGIVS--GYSMTPPTLSITTEESHVIDTGDSLSISCRGOHPL 58
 1 MESKVLLAVALWI, CVETRAAS VGLPSVSLDIPRISI-QKDILTIKANTTIQITCRGQRDL
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 Query Match 39.4%; Score 2797.5; DB 7; Length 1368; Best Local Similarity 44.6%; Pred. No. 1e-169; Matches 615; Conservative 204; Mismatches 472; Indels 89;
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RESULT 11 US-11-076-427A-10 'S Sequence 10, Application US/11076427A

```
GENERAL INFORMATION:
APPLICANT: Alicalo, et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU:
TITLE OF INVENTION: VESSEL ARTERIALIZATION
FILE REFERENCE: 28967/40008A
CURRENT APPLICATION NUMBER: US/11/076, 427A
CURRENT PILING DATE: 2005-03-08
PRIOR APPLICATION NUMBER: US 60/551,581
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.3
SEQ ID NO 10
LENGTH: 1363
 27;
 106
 518
 575
 638
 698
 163
 169
 223
 229
 283
 343
 346
 402
 403
 462
 462
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 687
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 758
 9
 58
 170 RSQSSVLWPDGQEVVWDDRRGMLVSTPLLHDALYLQCETTWGDQDFLSNPFLVHITGNEL
 1 MESKV1LAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 WLWPINNQSG-----SEQRVEVITECSDGL----FCKTLTIPKVIGNDTGAYKCFYR---
 --- ETDLASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCA
 224 YDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHOHKKLVNRDLKTQSGS
 347 AGDELVKLPVKLAAYPPPEFQWYKDGKALSGRH---SPHALVLKEVTEASTGTYTLALWN
 403 PISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQL
 463 EEEC----ANEPSQAVSVTNPYP-CEEWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLV
 463 WTPCKMFAQRSLRRRQQQDLMPQCRDWRAVTTQDAVNPIBSLDTWTEFVEGKNKTVSKLV
 519 IQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMQPTEQESVSLWCTADR
 523 IQNANVSAMYKCVVSNKVGQDERLIYFYVTTIPDGFTIESKPSEELLEGQPVLLSCQADS
 576 STFENLTWYKLGPQPLPIHVGELPTPVCKNLDTLWKLNATMFSNSTNDI-----LIM
 ELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLTVLERVAPTITGNLENQTTSIGESIEVS
 CTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAK
 284 EMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKNOSTFVRVHEKPFVAFGSGMESLVEAT
 344 VG-ERVRIPAKYLGYPPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTN
 RYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFCEAKINDESYQSIMYIVVVVGYRI
 Gaps
 92;
 Length 1363;
 Indels
 Query Match 38.9%; Score 2759; DB 7; Best Local Similarity 44.1%; Pred. No. 2.9e-167; Matches 608; Conservative 201; Mismatches 478;
Publication No. US20060025338A1
 TYPE: PRT
ORGANISM: Homo sapiens
 US-11-076-427A-10
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|---pdoea-edimlspltwedlvcysfqvargmeflasrkcihrdlaarnillsesdv 1050
 SLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNV 1041
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 CTASGNPPPQIMWFYDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAK 747
 YDIQLLPRKSLELLVGEKLVLNCTVWAEFNSGVTFDWDYPGKQAERGKWVPERRSQQTHT 289
 344 VG-ERVRIPAKYLGYPPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTN 402
 PISKEKQSHVVSLVVYVPPQIGEKSLISPVDSYQYGTTQTLTCTVYAIPPPHHIHWYWQL 462
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---ETDLASVIYVYVQDYRSPFIASVSDQHGVVYITENKNKTVVIPCLGSISNLNVSLCA 163
 SIPRVAPEHEGHYVCEVQDRRSHDKHCHKKYLSVQALEAPRLTQNLTDLLVNVSDSLEMQ
 LRSKRNEFVPYKTKG----ARFRQGKDYVGAIPVDLKR--RLDSITSSOSSASSGFVEEK
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 SLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNV 1041
 1042 VKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL 1101
 GASPYPGVKIDEBFCRRIKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLG 1161
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 YDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEBPBVKVIPDDNQTDSGMVLASEELKTLE 1273
 PDELPLDEHCERLPYDASKWEPPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAV 867
 KMLKEGATHSEHRALMSELKILLHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTY 927
 LRSKRNEFVPYKTKG----ARFRQGKDYVGAIPVDLKR--RLDSITSSQSSASSGFVEEK 981
 1274 DRTKLSPSFGGMVPSK----SRESVASEGSNQ--TSGYQSGYHSDDTDTTVYSSEEAEL 1326
 SRHRQESGFSCKGPGQNVAVTRAHPDSQGRRRRPERGARGG-----QVFYNSEYGEL 1340
 Sequence 121, Application US/11075047A
Publication No. US20060030000A1
GENERAL INPORMATION:
GENERAL INPORMATION:
TILE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
FILE REFRENCE: 28967/39700A
CURRENT APPLICATION NUMBER: US/11/075,047A
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/550,907
PRIOR FILING DATE: 2004-03-07
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin Version 3.2
SEQ ID NO 121
 WLWPNNOSG-----SEQRVEVTECSDGL----FCKTLTIPKVIGNDTGAYKCFYR--- 106
 MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLD
 92;
 DB 7; Length 1363;
 Query Match 38.9%; Score 2759; DB 7; Length 1 Best Local Similarity 44.1%; Pred. No. 2.9e-167; Matches 608; Conservative 201; Mismatches 478; Indels
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-047A-121
 RESULT 12
US-11-075-047A-121
 LENGTH: 1363
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 1230
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1213
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 982 SLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNV 1041
 S----PDOGA-EDLWLSPLTWEDLVCYSFOVARGMEFLASRKCIHRDLAARNILLSESDV 1050
 1230 YYNWVSFPGCLARGAETRGSSRMKTFEEFPM-TPTTYKGSVDNQTDSGWVLASEEFEGIE 1288
 1042 VKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSL 1101
 575
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 928 LRSKRNEFVPYKTKG----ARFRQGKDYVGAIPVDLKR--RLDSITSSQSSASSGFVEEK 981
 Sequence 6, Application US/11075047A

Sequence 6. Application US/11075047A

Publication No. US20060030000A1

GENERAL INFORMATION:

APPLICANT: ALITALO, et al.

TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS FILE REFERENCE: 28967/39700A

CURRENT APPLICATION NUMBER: US/11/075,047A

CURRENT FILING DATE: 2005-03-07

PRIOR APPLICATION NUMBER: US 60/550,907

PRIOR APPLICATION NUMBER: US 60/550,907

PRIOR FILING DATE: 2004-03-07

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PALENTIN Version 3.2

SEQ ID NO 6
 | :||::| ::||::|| ||||||||:|| 3583VAVEGSEDKGSMEIVILVGTGVIAVFFWVLLLLIFCNMRRPAHADIKTGYLSIIMD
 879 KMLKEGATASEHRALMSELKILIHIGNHLNVVNLLGACTKPQGPLMVIVEFCKYGNLSNF
 IQAANVSALYKCEAVNKVGRGERVISFHVTRGPE---ITLQPDMQPTEQESVSLWCTADR
 576 STFENLTWYKLGPQPLPIHVGELPTPVCKNLDTLWKLNATMFSNSTNDI-----LIM
 583 YKYEHLRWYRLNLSTLHDAHGNPLLLDCKNV----HLFATPLAASLEEVAPGARHATLSL
 ELKNASLQDQGDYVCLAQDRKTKKRHCVVRQLTVLERVAPTITGNLENQTTSIGESIEVS
 CTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVRKEDEGLYTCQACSVLGCAK
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 KMLKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTY
 748 VEAFFIIEGAQEKTNLEIIILVGTAVIAMFFWLLLVIILRTVKRANGGELKTGYLSIVMD
 1162 NLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVSCMEEEEVCDP-----KFH
 1214 YDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDSGMVLASEELKTLE
 1274 DRTKLSPSF 1282
 1289 SKHRQESGF 1297
 RESULT 14
US-11-075-047A-6
 519
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 Sequence 12, Application US/11076427A
Publication No. US20060025338A1
Publication No. US20060025338A1
GENERAL INFORMATION:
APPLICANT: Alitalo, et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU TITLE OF INVENTION: VESSEL ARTERIALIZATION
FILE REFERENCE: 28967/40008A
CURRENT APPLICATION NUMBER: US/11/076,427A
CURRENT FILING DATE: 2005-03-08
PRIOR APPLICATION NUMBER: US 60/551,581
PRIOR APPLICATION OF 33-08
NUMBER OF SEQ 1D NOS: 35
SOFTWARE: PatentIn version 3.3
 1230 YYNWVSFPGCLARGAETRGSSRWKTFEEFPM-TPTTYKGSVDNQTDSGWVLASEEFEQIE 1288
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| DLLQGRGLQEEEEVCWAPRS-SQSSEEGSFSQV9TWALHIAQADAEDSPPSLQRHSLAAR 1229
 1214 YDNTAGISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDSGMVLASEELKTLE 1273
 --KFH 1213
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 1274 DRIKLSPSFGGMVPSK----SRESVASEGSNQ--TSGYQSGYHSDDTDTTVYSSEEAEL 1326
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 WLWPINIQSG-----SEQRVEVTECSDGL----FCKTLTIPKVIGNDTGAYKCFYR--- 106
 229
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 VG-ERVRIPAKYLGYPPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDTGNYTVILTN 402
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Matches 597; Conservative 195; Mismatches 458;
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ORGANISM: Homo sapiens
 US-11-076-427A-12
 JS-11-076-427A-12
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 1230 YYNWVSFPGCLARGAETRGSSRMKTFEEFPM-TPTTYKGSVDNQTDSGMVLASEEFEQIE 1288
 GASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLG 1161
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 TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN TITLE OF INVENTION: PHOSPHATASE FILE REFERENCE: 06501-099002 CURRENT APPLICATION NUMBER: US/11/109,156 CURRENT FILING DATE: 2005-04-19
 PRIOR FILING DATE: ZOUG-01-22
PRIOR PELICATION NUMBER: PCT/7P00/05061
PRIOR PILING DATE: 2000-07-28
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PRIOR PLING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-211899
PRIOR PLING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-211899
PRIOR PLING DATE: 2000-06-09
 CURRENT FILING DATE: 2005-04-19
PRIOR APPLICATION NUMBER: US/10/060,065
PRIOR FILING DATE: 2002-01-29
 Sequence 23, Application US/11109156
Publication No. US20050250144A1
GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Takso Isogai
APPLICANT: Tetsuo Nishikawa
 Shizuko Ishii
Tomoyasu Sugiyama
Ai Wakamatsu
Kelichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
 Kaoru Otsuka
Jun-Ichi Yamamoto
 Chiaki Senoo
Jun-Ichi Nezu
 DRTKLSPSF 1282
 1289 SKHROESGF 1297
 Koji Hayashi
 SOFTWARE: Patentin Ver.
SEQ ID NO 23
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44.9%; Pred. No. 8.1e-167;
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 Conservative 195;
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ORGANISM: Homo sapiens
US-11-075-047A-6
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Best Local Similarity
Matches 597; Conserv
 LENGTH: 1298
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Service Services

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 6 LLAVALWICVETRAASVGLPSVSLDLPRISIQKDILTIKANTTLQITCRGQRDLDWLWPN
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1218 EKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEK 1039 1040 NVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIF SLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEH LGNLLQANAQQDGKDYIVLPISETLSMEEDSGLSLPTSPVS-CMEEEEVCDPKFHYDNTA 1219 GISQYLQNSKRKSRPVSVKTFEDIPLEEPEVKVIPDDNQTDSGMVLASEELKTL---EDR 1276 TKLSPSFGGMVPSKSRESVASEGSNQTSGYQS-GYHSDDTDTTVYSSEEAE 1325 924 1100 1160 8 g ઠે g 8 8 ⋧ ď ઠે g ò

Search completed: March 10, 2006, 19:07:58 Job time : 18.4695 secs

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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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 SUMMARIES
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 Post-processing: Minimum Match 0%
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92.2	91.9	91.8	89.9	89.3	88.4	76.7	71.7	6.69	67.2	44.1	43.9	43.6	43.3	43.3	42.7	42.4	42.3	42.0	42.0	
5542	5526.5	5518	5407.5	5371.5	5314	4612.5	4311	4203	4043	2652	2639.5	2623	2606	2603	2567	2550.5	2544	2527	2527	2000
S	92	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	2

## ALIGNMENTS

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 New tie-2 receptor tyrosine kinase and related nucleic acid - and methods for detecting tie-2 modulators for treating eg cancer, associated with
 This protein is the human homolog of mouse tie-2 receptor tyrosine kinase
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD 60
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD 60
 Gaps
 tie-2; receptor-tyrosine kinase; DNA primer; cancer; angiogenesis;
vasculogenesis; tek.
 .
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 Length 1124;
 0, Indels
 (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 DB 2;
 Query Match 100.0%; Score 6013; Best Local Similarity 100.0%; Pred. No. 0; Matches 1124; Conservative 0; Mismatches
 AAR73953 standard; protein; 1124 AA
 Disclosure; Page 49; 81pp; English
 Human TEK tyrosine kinase protein.
 angiogenesis and vasculogenesis.
 94WO-EP003767.
 93US-00152552
 22-JAN-1996 (first entry)
 WPI; 1995-194105/25.
 Sequence 1124 AA;
 Homo sapiens
 12-NOV-1994;
 12-NOV-1993;
 WO9513387-A1
 18-MAY-1995.
 AAR73953;
 Risau W;
AAR73953
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AAY30318 standard; protein; 1124

RESULT 2 AAY30318

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1020
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 999
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 FEALMNQHQDDLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 241 ICPPGFMGRTCEKACELHTFGRTCKERCSGQBGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 841 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVJCKLGHHPNIINLLGACEHRGYLYL
 961 IHRDLAARNILVGENYVAKIADFGLSRGGEVYVKKTWGRLPVRWMAIBSLNYSVYTTNSD
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNGVCHEDTGEC
 ICPPGFMGRTCEXACELHTFGRTCXERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTHRILPPDSG
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 901 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 IHRDLAARNILVGENYVAKIADFGLSRGOEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 QASFLPATLTMTVDKGDNVNI SFKKVLI KEEDAVI YKNGSFIHSVPRHEVPDILEVHLPH
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYBAWQHIQVTNBIVTLNYLBPRTBYBLCVQLVRRGEGGEGHPGPVRRFTTAS
 LLYKPVNHYBAWQHI QVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 541 IGLPPPRGLNLLPKSQTTLNLTWQPIPPSSEDDPYVEVERRSVQKSDQQNIKVPGNLTSV
 LLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSD1LPPQPEN1K1SN1THSSAV1SWT
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
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The present sequence represents the TEK protein, also known as TIEZ protein. TEK is a receptor tyrosine kinase. TEK contains epitopes which bind to MHC. The presentation of TEK epitopes can also stimulate helper cell and/or cytotoxic T cell responses. The immune response is directed against endothelial cells in the tumor-associated vasculature and consquiation and thrombosis. The immune response is targeted to coagulation and thrombosis. The immune response is targeted to coagulation and thrombosis. The immune response is targeted to conforthelial cells lining blood vessels of the tumor (these cells overexpress Tek), so damage to even a few cells will kill many tumor cells are accessable to the immune response and problems of antigenic heterogeneity, MHC loss and resistance to apoptosis (associated with epithelial cells) are unlikely to occur in normal condothelial cells. Tek spitopes (see AAX10320-24) are used to generate antibodies, and for prevention and treatment of cancer. The peptides, and recombinant DNA constructs or viral vectors that express them, are useful as anticancer vaccines to target endothelial cells that line blood
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 New peptides containing at least one epitope from Tek receptor tyrosine kinase, used in vaccines against cancer.
 61 FEALMNOHODPLEVTODVTREWAKKVVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 MDSLASIVICGVSLLLSGTVECAMDLILINSLPIVSDAETSLTCIASGWRPHEPITIGRD
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 Gaps
 TEK protein; TIE2 protein; receptor tyrosine kinase; T cell resp
immune response; endothelial cell; tumor-associated vasculature;
coagulation; thrombosis; cancer; anticancer vaccine.
 ;
0
 Length 1124;
 Indels
 Amino acid sequence of TEX (also known as TIE2) protein
 ;
 Hewett PW, Ramage JM.
 DB 2;
 100.0%; Score 6013;
100.0%; Pred. No. 0;
ive 0; Mismatches
 (CANC-) CANCER RES CAMPAIGN TECHNOLOGY
 Disclosure, Fig 1, 56pp, English
 99WO-GB000583
 98GB-00004121
 Spendlove I,
 Matches 1124; Conservative
 vessels of the tumor
 WPI; 1999-540586/45.
 Similarity
 Sequence 1124 AA;
 26-FEB-1999;
 26-FEB-1998;
 Homo sapiens
 WO9943801-A1
 15-NOV-1999
 Durrant LG,
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 181
 Query Match
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/note= "catalytic domain; specifically claimed fragment"

Location/Qualifiers

Homo sapiens

802. .1124

Domain

WO200172778-A2

04-OCT-2001

20-MAR-2001; 2001WO-US008853 29-MAR-2000; 2000US-0192920P

(BADI ) BASF AG

Tie-2; catalytic domain; receptor tyrosine kinase; crystalline; human; cytostalic; vasotropic; antianemic; antiarteriosclerotic; nephrotropic; opthalmological; hepatotropic; antithyroid; antiinflammatory; antiulcer; gastrointestinal; antirheumatic; osteopathic; antiarthritic; hemostatic; antipsoriatic; dermatological; immunosuppressive; antibacterial.

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AQPQDAGVYSARY I GGNLFTSAFTRLI VRRCEAQXWGPECNHLCTACMNNGVCHEDTGEC
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNPAVINISSEPYFGDGPIKSKK
 LINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 SNPAPSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 ARI KKDGLRMDAAI KRMKEYASKDDHRDFAGELEVLCKLGHHPNI INLLGACEHRGYLYL
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIBSLNYSVYTTNSD
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNPAVINISSEPYFGDGPIKSKK
 LLYKPVNHYBAWQHIQVTNBIVTLNYLBPRTBYBLCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSOTTLNLTWOP1 PPSSEDDFYVEVERRSVOKSDOONI KVPGNLTSV
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 LLNNLHPREOYVVRARVNTKAOGEWSEDLTAWTLSDILPPOPENIKISNITHSSAVISWT
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK
 ARIKKDGLRMDAAIKRMKEYASKDDHRDPAGELEVICKLGHHPNIINLLGACEHRGYLYL
 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
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The invention relates to a crystalline polypeptide, comprising the catalytic domain of a receptor tyrosine kinase Tie-2 protein. The crystalline forms are useful for identifying inhibitors of a Tie-2 protein as well as determining the three dimensional structure of a the catalytic domain of a Tie-2 polypeptide. A Tie-2 inhibitor may be used to treat a Tie-2 dependent condition in a patient (especially a human), where the condition is characterized by excessive vascular proliferation e.g. a hyperproliferative disorder, cancer (e.g. sarcoma, osteoma, nelanoma, lymphoma, and leukemia), a cardiovascular condition (e.g. anteroscierosis, ischemia, anemia, and vascular leakage disorders), an cular condition (myopia, chronic retinal detachment, conjunctivitis, certinopathy, and macular degeneration), von Hippel Lindau disease, pemphigoid, psoriasis, Paget's disease, polycystic kidney disease, pemphigoid, psoriasis, Paget's disease, polycystic kidney disease, chronic inflammation, synovitis, inflammatory bowel disease, Crohn's chemic inflammation, synovitis, inflammatory bowel disease, Crohn's chemic or sepsis, especially where the disorder involves aberrant endochelial interactions. The Tie-2 inhibitor may be used to decrease fertility, and promote angiogenesis or vasculogenesis (in combination with a pro-angiogenic growth factor). The present sequence
 ö
 120
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 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDABTSLTCIASGWRPHEPITIGRD
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 QASFLPATLTWTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 Crystalline polypeptide useful for identifying inhibitors of a Tie-2 protein as well as determining the three dimensional structure of a polypeptide comprising the catalytic domain of a Tie-2 polypeptide.
 Gaps
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 Length 1124;
 Indels
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 Hoeffken HW,
 Score 6013; I
Pred. No. 0;
; Mismatches
 RW,
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 Claim 6; Fig 1; 242pp; English
 100.0%;
 Dixon
 Best Local Similarity 100.
Matches 1124; Conservative
 Arnold LD,
 WPI; 2001-648437/74.
 Similarity
 Sequence 1124 AA
 Bellamacina C;
 19
 Query Match
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Amino acid sequence of human Tie-2.

11-FEB-2002

AAG65945;

AAG65945 ID AAG6 XX AAC AC AAG6 XX II-F XX DE Amin

AAG65945 standard; protein; 1124

RESULT 3

Human Tie2 receptor tyrosine kinase protein

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1020
 1021 VWSYGVILWEIVSLGGTPYCCMTCAELYEKLPQGYRLEKPINCDDEVYDLMRQCWREKPY 1080
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY 1080
 240
 300
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 360
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 420
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 480
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 540
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 99
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 720
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 780
 840
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 960
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 AQPQDAGVYSARYIGGNIFITSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLOCNE
 VWVCSVNTVAGMVEKPPNISVKVLPRPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLNLTWQPIPPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 SNPAFSHELVTLPESQAPADLGGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 ARIKKDGLRMDAAIKRMXEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNI INLLGACEHRGYLYL
 AIEYAPHGNILLDFLIKKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQXQF
 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPFN1SVKVLPKPLNAPNV1DTGHNFAV1N1SSEPYFGDGP1KSKK
 LLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVBVERRSVQKSDQQNIKVPGNLTSV
 LLINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 LINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 ILDGYSISSITIRYKVÓGKNEDŐHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK
 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQXQF
 ERPSFAOILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
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(first entry)

18-JUN-2002

**EXXXEX** 

AAU78550 AAU78550;

AAU78550

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 120
 61 FEALMNOHODPLEVTODVTREWAXKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKWRQ 120
 180
 Tie2; Tie2K; human; crystal structure; vascular dysmorphogenesis;
protein co-ordinate data; receptor tyrosine kinase; vascular development.
 Composition for the design or screening of a cytoplasmic Tie2 receptor tyrosine kinase domain modulator, comprises a monoclinic or orthorhombic crystalline form of a cytoplasmic Tie2 receptor tyrosine kinase domain polypeptide.
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 This invention relates to the 3 dimensional crystal structure of the human Tie2 receptor tyrosine kinase domain polypeptide in a monoclinic, or orthorhombic crystalline form. Tie2 is an endothelial-specific receptor tyrosine kinase thought to be involved in vascular development. Naturally occuring R849W and Y897S mutations in the Tie2 protein have been identified in human s and have been shown to segregate with the autosomal dominant condition vascular dysmorphogenesis. The invention also comprises methods for designing modulators of the biological activity of the cytoplasmic Tie2 receptor tyrosine kinase domain. The Tie2 receptor tyrosine kinase domain is used to design or screen for a modulator of the kinase by rational drug design, using computer models. The present sequence represents the human Tie2 protein used to create th Tie2K tyrosine kinase domain of the invention
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 FEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 Gaps
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 Length 1124;
 Shewchuk LM;
 Indels
 808. .1124
/note= "Tie2K receptor kinase domain"
 /note= "Catalytic aspartate residue"
 DB 5;
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 WD.
 982. .1008
/note= "Activation loop"
1119
/note= "Phosphorylation site"
 note= "Phosphorylation site'
 100.0%; Score 6013;
100.0%; Pred. No. 0;
tive 0; Mismatches
 Holmes
 Disclosure; Page 565-570; 581pp; English.
 832. .836
/note= "ATP binding
 .ocation/Qualifiers
 Hassell AM,
 06-SEP-2001; 2001WO-US027486
 08-SEP-2000; 2000US-0231398P
 Matches 1124; Conservative
 Davis RG, Ellis BP,
 964
 (GLAX) GLAXO GROUP
 897
 WPI; 2002-292263/33.
 Similarity
 Sequence 1124 AA;
 N-PSDB; ABK12246.
 WO200220734-A2
 Binding-site
 Homo sapiens
 14-MAR-2002
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 Query Match
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us-10-633-742-8.rag

(first entry)

16-MAY-2002

240 240 300 300 360

360 420 420 480 540 540 009 909

480

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QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH 180
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 ACHPGFYGPDCKLRCSCNNGEMCDRPQGCLCSPGWQGLQCEREGIPRWTPKIVDLPDHIE
 LLYKPVNHYBAWQHIQVTNBIVTLNYLEPRTEYELCVQLVRRGEGGBGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSBDDFYVBVBRRSVQKSDQQNIKVPGNLTSV
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 MAQA FQNVREEPA VQFNSGTLALNRKVKNNPDPTI YPVLDWNDI KFQDVIGEGNFGQVLK
 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLWRQCWREKPY
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNGVCHEDTGEC
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 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPBCNHLCTACMNNGVCHEDTGBC
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVBVERRSVQKSDQQNIKVPGNLTSV
 LINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 ERPSFAQILVSLNRMLBERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
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Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; themazoid arthritis; mycoardial infarction; thrombophlebitis; umour angiogenesis; breast carcinoma; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
 Paoni NF;
 One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
 S
 ABL88072 to ABL88258 encode the PRO proteins given in ABB84817
 Goddard A;
 PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, IP, Watanabe CK, Williams PM, Wood WI, Ye W;
 Gerritsen ME,
 Human PRO734 protein sequence SEQ ID NO:82
 Gerber H,
 Claim 11; Fig 82; 565pp; English
 2000WO-US030952.
2000WO-US030873.
2000WO-US032678.
2000US-00747259.
2000WO-US034956.
 2001WO-US006520.
2001WO-US00666.
2001US-00802706.
2001US-00808689.
2001US-00816744.
2001US-00853366.
 2001US-00854280.
2001US-00866028.
2001US-00866034.
 2000US-0220664P.
2000WO-US020710.
 2000WO-US023522.
2000WO-US023328.
2000US-0230978P.
 2000US-00665350
2000US-0242922P
 20-JUN-2001; 2001WO-US019692
 2000US-00664610
 2000US-00709238
 2001US-00767609
 2001US-00796498
 2001WO-US017092
2001US-00870574
 2001WO-US017443
2001WO-US017800
 2000US-00643657
 Ferrara N,
 (GETH) GENENTECH INC
 WPI; 2002-090516/12.
 N-PSDB; ABL88112
 WO200200690-A2
 17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
07-SEP-2000;
 18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
08-NOV-2000;
10-NOV-2000;
10-DEC-2000;
20-DEC-2000;
20-DEC-2000;
22-JAN-2001;
28-FEB-2001;
01-MAR-2001;
01-MAR-2001;
14-MAR-2001;
25-AMR-2001;
14-MAR-2001;
16-AMR-2001;
16-AMR-2001;
 10-MAY-2001;
25-MAY-2001;
25-MAY-2001;
 25-JUL-2000;
28-JUL-2000;
02-AUG-2000;
 Homo sapiens
 01-JUN-2001;
 30-MAY-2001;
 20-JUL-2000;
25-JUL-2000;
 Stephan JF,
 25-MAY-2001;
 30-MAY-2001
 03-JAN-2002
 Baker KP,
 Godowski
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ABB84857 standard; protein; 1124

ABB84857

ABB84857 ID ABBE XX AC ABBE

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ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABU88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
 781 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK 840
 9
 9
 241 ICPPGFMGRTCEKACELHTFGRTCKERCSGQBGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 PEALANQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 FEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNGVCHEDTGEC
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMYEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYBAWQHIQVTNBIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYBAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPXSQTTLNLTWQPIFPSSEDDFYVEVERRSVQXSDQQNIXVPGNLTSV
 541 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 LLINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 1LDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
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 DB 5; Length 1124;
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 100.0%; Score 6013;
100.0%; Pred. No. 0;
tive 0; Mismatches
 Best Local Similarity 100.
Matches 1124; Conservative
 Sequence 1124 AA;
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1080 840 900 900 960 960 Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic. ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL 901 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF 961 IHRDIAARNILVGENYVAKIADFGLSRGOEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1021 VWSYGVLAMEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL AIEXAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF 1HRDLAARN1LVGENYVAK1ADFGLSRGQEVYVKKTMGRLPVRWMA1ESLNYSVYTTNSD VWSYGVILUWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPINCDDEVYDLMRQCWREKPY ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124 Human angiogenesis related protein PRO734 SEQ ID NO: 82 Z ABB95463 standard; protein; 1124 2000US-0230978P 2000US-00664610 2000US-0242922P 2000WO-US030873. 2001US-00816744 2001US-00828366 09-JUL-2001; 2001WO-US021735 2000WO-US020710 2000WO-US023328 2000US-00665350 2000WO-US030952 -00747259 2000WO-US034956 2001US-00767609 2001US-00796498 2001WO-US006520 2001WO-US006666 2000WO-US023522 2000US-00643657 19-JUL-2002 (first entry) 2000US-WO200208284-A2 02-AUG-2000; 17-AUG-2000; 23-AUG-2000; 24-AUG-2000; 07-SEP-2000; 22-JAN-2001; 28-FEB-2001; 28-FEB-2001; 10-NOV-2000; 01-DEC-2000; 20-DEC-2000; 24-OCT-2000; 08-NOV-2000; 08-NOV-2000; 22-MAR-2001; 05-APR-2001; 28-JUL-2000; 18-SEP-2000; 20-DEC-2000; 31-JAN-2002 841 841 901 1081 781 961 1021 ABB95463 Homo RESULT 6 ABB95463 ⋧ g à 임 à 셤 ઠે 셤 ò 셤  -

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961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1020
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 909
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 241 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE 300
 361 VNSGKENPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNFTDHFSVAIFTIHRILPPDSG
 ARIKKOGLRADAAIKRAKEYASKODHROFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRMMAIESLNYSVYTTNSD
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYEAWQHIQVTNEIVTLEPRIEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGWTCLTVLLAFLILQLKRANVQRR
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 661 ILDGYSISSITIRYKVQSKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 AIEYAPHGNILDFIRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 V#VCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LINNIHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK
 VWSYGVLLWEIVSLGGTPXCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 1021 VWSYGVILWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 Human; angiogenesis-associated transcript; angiogenesis; angiogenesis-associated disease; cancer; cytostatic.
 Angiogenesis-associated human protein sequence #73
 Ş
 ABU03528 standard; protein; 1124
 (first entry)
 Homo sapiens
 361
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 The present invention provides the protein and coding sequences of human cardiovascular. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thrombophlebitis, lymphangitis, tunmour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention
 61 FEALMYQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ 120
 QASFLPATLIMIYDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH 180
 9
 9
 241 ICPPGFWGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 121 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 FEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRO
 181 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 One hundred and eighty seven nucleic acids encoding PRO polypeptides useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
 Gaps
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 5; Length 1124;
 Indels
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 100.0%; Score 6013;
100.0%; Pred. No. 0;
ative 0; Mismatches
 Claim 11; Fig 82; 567pp; English.
10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

25-MAY-2001; 2001US-00866034.

25-MAY-2001; 2001WS-00866034.

25-MAY-2001; 2001WS-00870574.

30-MAY-2001; 2001WS-00870574.

30-JUN-2001; 2001WS-US017493.
 2001WO-US019692
 Query Match 100.
Best Local Similarity 100.
Matches 1124; Conservative
 GENENTECH INC.
BAKER K P.
FERRARA N.
 GERBER H.
GERRITSEN M E.
GODDARD A.
 GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
 PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
 2002-171999/22
 WOOD W I.
 Sequence 1124 AA;
 N-PSDB; ABL95601
 20-JUN-2001;
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(WALL)
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 (GETTH)
(BAKE/)
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The present invention relates to methods and compositions for detecting an angiogenesis-associated transcript in a cell in a patient. The method involves contracting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence at least 80% identical to any of the angiogenesis-associated human polymucleotide sequences given in the specification. These angiogenesis-associated polymucleotide sequences comprise genes that exhibit changes in expression levels as a function of time in tissue undergoing capressis. The method and the polymucleotide sequences of the invention are useful for diagnosing and treating angiogenesis and angiogenesis-associated diseases e.g. cancer. The polymucleotide sequences concerned in the gene therapy of such disorders. The sequences are also useful in the gene therapy of such disorders. The sequences are also useful in the gene therapy of such disorders. The sequences are useful as a vaccine for therapeutic and prophylactic immunisation. ABU03456-ABU03569 represent anglogenesis-associated disorders are useful as a vaccine for therapeutic and prophylactic immunisation.
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 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIB 360
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ 120
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH 180
 9
 9
 Detecting angiogenesis-associated transcript in a cell for diagnosing treating cancer by contacting a sample with a polynuclectide that exhibits changes in expression level as a function of time in tissue undergoing angiogenesis.
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNGVCHEDTGEC
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 I CPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 AQPQDAGVYSARY IGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 Gaps
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 Length 1124;
 Indels
 DB 6;
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 100.0%; Score 6013;
100.0%; Pred. No. 0;
tive 0; Mismatches
 Aziz N;
 Example 2; Page 250; 291pp; English.
 Glynne R, Watson SR,
 (EOSB-) EOS BIOTECHNOLOGY INC
 22-FEB-2001; 2001US-00791390.
19-APR-2001; 2001US-0285475P.
03-AUG-2001; 2001US-0350666F.
13-NOV-2001; 2001US-0350666F.
 29-NOV-2001; 2001US-0334244P
 2002WO-US004915
 Best Local Similarity Love.
Matches 1124; Conservative
 WPI; 2003-040681/03
 Query Match
Best Local Similarity
 Sequence 1124 AA;
 N-PSDB; ABX08812
 WO200279492-A2
 14-FEB-2002;
 10-OCT-2002
 Murray R,
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 Cytostatic, vasodilator; antiinflammatory; cardiant; gene therapy; ligand-receptor binding modulator; ephrin ligand; angiogenesis; lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder; ell migration disorder; cell proliferation disorder; neovascularisation; ischaemia; infarction; tissue graft; transplant; human; tie 2; tie receptor tyrosine kinase 2; enzyme.
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 361 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 781 MAQAFQNVREEPAVQFNSGTLALNRKVKONNPDPTIYPVLDMNDIKFQDVIGEGNFGQVLK
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTWGRLPVRWMAIESLNYSVYTTNSD
 1021 VWSYGVLAMEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 V#VCSVNTVAG#VEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 LLYKPVNHYEAWOHI OVTNEIVTLNYLEPRTEYELCVOLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGINILIPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 LINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 661 ILDGYSISSITIRYKVOGKNEDOHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MAQAFONVREEPAVQFNSGTLALNRKVKNNPDPT1YPVLDWND1KFQDV1GEGNFGQVLK
 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 901 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGP1KSKK
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 LLINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 1081 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 ERPSPAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 Human Tie receptor tyrosine kinase 2 (Tie 2).
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 ABU07838 standard; protein; 1124
 (first entry)
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 10-MAY-2003
 1021
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IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1020
 1021 VWSYGVLAMEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY 1080
 human; secreted protein, transmembrane protein, cardiovascular disorder; endothelial disorder; anglogenic disorder; myocardial infarction; cardiac hypertrophy; tranma; cancer; age-related macular degeneration; anglogenesis; endothelial cell apoptosis; smooth muscle cell growth; endothelial cell tube formation.
 MAQAFQNVREEPAVQPNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK
 ARIKKOGLRMDAAIKRMKBYASKODHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYBAWQHIQVTNBIVTLNYLEPRTBYBLCVQLVRRGEGGEGHPGPVRRFTTAS
 LLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVBVERRSVQKSDQQNIKVPGNLTSV
 541 IGLPPPRGLNLLPRSOTTLNLTWOPIPPSSEDDFYVEVERRSVOKSDOONIKVPGNLTSV
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK
 ARIKKOGLRADAAIKRMKEYASKODHRDFAGELEVICKI,GHHPNI INLIGACEHRGYLYL
 AIBYAPHGNILDPLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 901 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 LLINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 VWSYGVILWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEBA 1124
 Human secreted/transmembrane PRO polypeptide #41.
 ADD10371 standard; protein; 1124 AA
 16-AUG-2002; 2002US-00223084.
 15-SEP-2000; 2000US-0232887P.
 01-JAN-2004 (first entry)
 US2003105011-A1.
 541
 661
 721
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 841
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 ADD10371;
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 The invention describes a method of identifying a modulator of binding between a Tie receptor tyrosine kinase and an Ephrin ligand. The method composition in the presence and in the absence of a putative modulator composition in the presence and in the absence of the putative modulator. The method is useful for identifying a modulator of binding between a Tie receptor and the Ephrin tyrosine kinase and an Ephrin ligand. Modulators identified from the cyrosine kinase and an Ephrin ligand. Modulators identified from the tyrosine kinase and an Ephrin ligand. Modulators identified from the cyrosine kinase and an Ephrin ligand. Modulators identified from the tyrosine kinase and an Ephrin ligand. Modulators identified from the cyrosine kinase and an Ephrin ligand. Modulators identified from the tyrosine kinase and an Ephrin gasease associated with aberrant Ephrin-compound, aberrant growth, migration or proliferation of calls that express a Tie receptor, or for promoting growth of vessel or cheomic compound, or a tissue graft or transplant). This is the amino character of human Tie receptor tyrosine kinase 2 (Tie 2)
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 120
 180
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 FEALMNQHQDFLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKWRQ 120
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK 480
 Identifying modulators of binding between a Tie receptor tyrosine kinase and an Ephrin ligand, useful for promoting neovascularization, comprises contacting a Tie receptor with an Ephrin in the presence of a putative
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 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGND
 241 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 QASFLPATLTMTVDKGDNVNI SPKKVLIKEEDAVI YKNGSFIHSVPRHEVPDILEVHLPH
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNGVCHEDTGEC
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACANNGVCHEDTGEC
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCBREGIPRMTPKIVDLPDHIE
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 361 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIPTIHRILPPDSG
 Gaps
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 Query Match 100.0%; Score 6013; DB 6; Length 1124; Best Local Similarity 100.0%; Pred. No. 0; Matches 1124; Conservative 0; Mismatches 0; Indels 0;
 Example 1; Page 72-76; 199pp; English.
 02-JUL-2002; 2002WO-IB002524
 02-JUL-2001; 2001US-0302960P.
 (LICH) LICENTIA LTD
 WPI; 2003-210341/20
N-PSDB; ABX12539.
 Alitalo K, Kubo H;
 Sequence 1124 AA;
WO2003004529-A2
 16-JAN-2003
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20-JUN-2001; 2001WO-US019692.
09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
 US2003105013-A1
 Homo sapiens
 01-JAN-2004
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 transmembrane polypeptide (PRO). The nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiosenic disorder in a mammal. preferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO1499 is used to stimulate angiogenesis. PRO4302 or an agonist is used to induce andothelial cell apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to induce endothelial cell upoptosis. A propartrophy endother south muscle cell growth, or to induce endothelial cell tube formation. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention.
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 New isolated nucleic acid encoding a secreted and transmembrane polypeptide for treating a cardiovascular, endothelial, or angiogenic disorder in a mammal, such as cancer or age-related macular degeneration.
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 Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PM, Wood WI, Ye W;
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 ACHPGFYGFDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VNSGKENPICKASGWPLPTNBEMTLVKPDGTVLHPKDFNHTDHFSVAIFTHRILPPDSG
 V#VCSVNTVAG#VEKPPNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 QASFLPATLTWTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNGVCHEDTGEC
 I CPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 I CPPGFMGRITCEKACELHTFGRITCKERCSGOEGCKSYVFCLPDPYGCSCATGWKGLOCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKI NGAYFCEGRVRGEAIRIRTMKMRQ
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
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 Gaps
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0
 7; Length 1124;
 0; Indels
 8
 100.0%; Score 6013;
100.0%; Pred. No. 0;
iive 0; Mismatches
 Claim 11; SEQ ID NO 82; 493pp; English
20-JUN-2001, 2001WO-US019692.
09-JUL-2001, 2001WO-US021735.
20-FEB-2002, 2002US-00081056.
 Godowski PJ, Gurney AL, H
Watanabe CK, Williams PM,
 Matches 1124; Conservative
 Ferrara N,
 (GETH) GENENTECH INC.
 WPI; 2003-810831/76.
N-PSDB; ADD10370.
 Similarity
 Sequence 1124 AA;
 Baker KP,
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 human; secreted protein; transmembrane protein; cardiovascular disorder; endothelial disorder; angiogenic disorder; myocardial infarction; cardiac hypertrophy; tranuma; cancer; age-related macular degeneration; angiogenesis; endothelial cell apoptosis; smooth muscle cell growth; endothelial cell tube formation.
 LLYKPVNHYBAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 901 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTWGRLPVRWMAIESLNYSVYTTNSD
 1021 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
LLYKPVNHYEAWOHI OVTNEI VTLNYLEPRTEY ELCVOLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 LLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPT1YPVLDWND1KFQDV1GEGNFGQVLK
 781 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK
 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 A I EYAPHGNLLDFLRKSRVLETDPAFAI ANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 1021 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 Human secreted/transmembrane PRO polypeptide #41.
 Ą
 ADD11331 standard; protein; 1124
 16-AUG-2002; 2002US-00223090
 (first entry)
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US2003105012-A1
 15-SEP-2000; 2
20-JUN-2001; 2
09-JUL-2001; 2
20-FEB-2002; 2
 Homo sapiens
 15-JAN-2004
 05-JUN-2003
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 transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded transmembrane polypeptide (PRO). The nucleic acid, or an agonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, proferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial cell growth in a mammal. PRO10 or an agonist is used to stimulate angiogenesis. PRO4102 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO149 is used to stimulate angiogenesis. A PRO polypeptide, given in the specification, or an agonist is used to induce endothelial cell tube formation. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention.
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 120
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 180
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 300
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 360
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 420
 420
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 481 LLYKPVNHYBAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGFVRRFTTAS 540
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 Stephan JF
 New isolated nucleic acid encoding a secreted and transmembrane polypeptide, useful for treating a cardiovascular, endothelial, or angiogenic disorder in a mammal, such as cancer or age-related macular
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 QASFLPATLIMITVDKGDNVNISPKKVLIKEEDAVIYKNGSPIHSVPRHEVPDILEVHLPH
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHPSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 FEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTWKMRQ
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIR
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
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 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 QASFLPATLTMTVDKGDNVNI SPKKVLI KEEDAVI YKNGSFIHSVPRHEVPDI LEVHLPH
 VWVCSVNTVAGMVEXPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 Gaps
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 7; Length 1124;
 Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J,
PM, Wood WI, Ye W;
 0; Indels
 OB
 100.0%; Score 6013;
100.0%; Pred. No. 0;
ive 0; Mismatches
 Claim 11; SEQ ID NO 82; 493pp; English
 Gurney AL, H
 Best Local Similarity 100.
Matches 1124; Conservative
 Ferrara N,
 (GETH) GENENTECH INC
 WPI; 2003-801242/75.
N-PSDB; ADD11330.
 Sequence 1124 AA;
 Godowski PJ,
Watanabe CK,
 degeneration.
 Baker KP,
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961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1020
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 human; secreted protein; transmembrane protein; cardiovascular disorder; endothelial disorder; angiogenic disorder; myocardial infarction; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 IGLPPPRGLNLLPKSQTTLNLTWQPIPPSSEDDPYVEVERRSVQKSDQQNIKVPGNLTSV
 661 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPT1YPVLDWND1KFQDV1GEGNFGQVLK
 ARIKKOGLRMDAAIKRMKEYASKODHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 1021 VWSYGVILWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPINCDDBVYDLMRQCWREKPY
LLYKPVNHYEAWQH1QVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLNLTWQPIPPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 1LDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 VWSYGVLLWEIVSLGGTPYCGMTCAELYBKLPQGYRLBKPLNCDDEVYDLMRQCWREKPY
 ERPSFAQILVSLNRMLBERKTYVNTTLYBKFTYAGIDCSAEBAA 1124
 Human secreted/transmembrane PRO polypeptide #41.
 Z
 ADD37124 standard; protein; 1124
 endothelial cell tube formation.
 2000US-0232887P.
2001WO-US019692.
2001WO-US021735.
2002US-00081056.
 16-AUG-2002; 2002US-00223088
 (first entry)
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Human kinase TIE2
 WO2003081210-A2
 Prescott JC,
 12-FEB-2004
 02-OCT-2003
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 transmembrane polypeptide (PRO). The nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, preferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial prowth in a mammal. PRO21 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO4149 is used to stimulate angiogenesis. PRO4102 or an agonist is used to induce endothelial cell apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to stimulate or inhibit smooth muscle cell growth, or to induce endothelial cell tube formation. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention.
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 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE 360
 polypeptide for treating a cardiovascular, endothelial, or angiogenic
disorder in a mammal, such as cancer or age-related macular degeneration.
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 Stephan JF;
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDABTSLTCIASGWRPHEPITIGRD
 FEALMNOHODPLEVIODVIREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKWRO
 181 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTHRILPPDSG
 VWVCSVNTVAGMVEKPFNI SVKVLPKPLNAPNVI DTGHNFAVINI SSEPY FGDGPIKSKK
 LLYKPVNHYBAWOHI OVTNBI VTLAYLEPRTEY ELCVOL VRGEGGEGHPGPVRRFTTAS
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 AQPODAGVYSARY I GGNL FTSAFTRL I VRRCEAOKWGPECNHLCTACMNNGVCHEDTGEC
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 Gaps
 New isolated nucleic acids encoding a secreted and transmembrane
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 DB 7; Length 1124;
 Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J,
PM, Wood WI, Ye W;
 Indels
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 100.0%; Score 6013;
100.0%; Pred. No. 0;
iive 0; Mismatches
 Claim 11; SEQ ID NO 82; 492pp; English.
 Godowski PJ, Gurney AL, H
Watanabe CK, Williams PM,
 Best Local Similarity 100.
Matches 1124; Conservative
 Ferrara N,
(GETH) GENENTECH INC
 2003-829354/77.
 Sequence 1124 AA;
 N-PSDB; ADD37123
 Baker KP,
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 Query Match
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 1021 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY 1080
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 780
 780
 840
 840
 900
 900
 960
541 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 841 ARIKKOGLRADAAIKRMKEYASKODHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAPSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK
 841 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 901 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 901 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQXQF
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLFVRWMAIESLNYSVYTTNSD
 LLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSD1LPPQPEN1K1SN1THSSAV1SWT
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 1081 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 Human; protein kinase; enzyme; inhibitor; TIS2.
 ADF45095 standard; protein; 1124 AA.
 20-MAR-2003; 2003WO-US008725
 21-MAR-2002; 2002US-0366892P
 (SUNE-) SUNESIS PHARM INC
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 WPI; 2003-865136/80.
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 The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.
 1 MDSLASLVLCGVSLLLSGTVBGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 ICPPGFMGRTCEKACELHTFGRTCKBRCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPPNISVKVLPKPLNAPNVIDTGHNPAVINISSEPYFGDGPIKSKK
 V#VCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVMHY EAWQHIQVTNEIVTLMYLEPRTEYELCVQLVRRGEGGEGHPGPVRFFTTAS
 541 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 QASFLPATLTWTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNGVCHEDTGEC
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 LLYKPVNHYBAWQHIQVTNBIVTLNYLBPRTEYBLCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLLNLTWQPIPPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 LLINNI, HPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 661 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 Gaps
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 DB 7; Length 1124;
 Indels
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 Query Match 100.0%; Score 6013; Best Local Similarity 100.0%; Pred. No. 0; Matches 1124; Conservative 0; Mismatches
 Disclosure; SEQ ID NO 64; 260pp; English.
 kinase-ligand conjugate formation.
 Sequence 1124 AA;
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 The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal,
 human; secreted protein; transmembrane protein; cardiovascular disorder; andochelial disorder; angiogenic disorder; myocardial infarction; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 Gerber H, Gerritsen ME, Goddard A;
L, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PM, Wood WI, Ye W;
 New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or PRO214, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and for treating disorders involving
 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 961 IHRDLAARNILVGENYVAKIADFGLSRGGEVYVKKTWGRLPVRWAIESLNYSVYTTNSD
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPT1YPVLDWND1KFQDV1GEGNFGQVLK
 ARIKKDGLRMDAAIKRMKBYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 ERPSFAQILVSLNRMLBERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 secreted/transmembrane PRO polypeptide #41.
 Claim 11; SEQ ID NO 82; 492pp; English.
 Ź
 Godowski PJ, Gurney AL, Hillan
Watanabe CK, Williams PM, Wood
 ADE41332 standard; protein; 1124
 cell tube formation.
 20-JUN-2001; 2001WO-US019692.
09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
 16-AUG-2002; 2002US-00223085
 (first entry)
 (GETH) GENENTECH INC.
 Ferrara N,
 WPI; 2004-008957/01.
 N-PSDB; ADE41331.
 US2003100497-A1.
 Homo sapiens
 angiogenesis
 endothelial
 29-MAY-2003
 Baker KP,
 841
 841
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 ADE41332;
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781 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPT1YPVLDWND1KFQDV1GEGNFGQVLK

ARI KKOGLRMDAAI KRMKEYASKODHRDFAGELEVLCKLGHHPNI INLLGACEHRGYLYL

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901 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF AIEYAPHGNILDFIRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD VWSYGVILWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY 1021 VWSÝGVLLWEIVSLGGTPÝCGMTCABLÝEKLÞQGYRLEKPINCDDEVYDLMRQCWREKPY

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preferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial chypertrophy. PRO1376 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO149 is used to stimulate angiogenesis. PRO4302 or an agonist is used to induce endothelial angiogenesis polypeptide, given in the specification, or an agonist is used to stimulate or inhibit smooth muscle cell growth, or to induce endothelial cell tube formation. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention.
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 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCTASGWRPHEPITIGRD
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 QASFLPATLTMTVDKGDNVNI SFKKVLI KEEDAVI YKNGSFIHSVPRHEVPDILEVHLPH
 QASFLPATLIMITVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 ICPPGFMGRICEKACELHIFGRICKERCSGQEGCKSYVFCLPDPYGCSCAIGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 V#VCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 AQPQDAGVYSARY1GGNLFTSAFTRL1VRRCEAQXWGPECNHLCTACMNGVCHEDTGEC
 AQPQDAGVYSARYIGGNLFISAFIRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDIGEC
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 VNSGKFNPI CKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAI FTIHRILPPDSG
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 LLYKPVNHYEAWQHIQVTNBIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSOTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 Gaps
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 Length 1124;
 0; Indels
 DB 8;
 100.0%; Score 6013;
100.0%; Pred. No. 0;
 0; Mismatches
 Matches 1124; Conservative
 Local Similarity
 Sequence 1124 AA;
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useful The invention relates to human PRO polypeptides and the PRO polymucleotides encoding them. The invention also relates to treating cardiovascular, endothelial or angiogenic disorders in mammals, inhibiting endothelial cell growth, stimulating endothelial cell growth, stimulating endothelial cell growth, stimulating endothelial cell growth, stimulating endothelial cell growth stimulating angiogenessis or smooth muscle cell growth by administering polypeptides of the invention. The PRO polypeptides and polymucleotides are useful for treating cardiovascular, endothelial or anglogenic New PRO polypeptides and nucleic acids encoding the polypeptides, useful for treating myocardial infarction, cardiac hypertrophy, trauma, cancer, or age-related macular degeneration. Paoni NF; Human; PRO; cardiovascular disorder; endothelial disorder; angiogenic disorder; endothelial cell growth; cardiac hypertrophy; cell apoptosis; cell tube formation; angiogenesis; smooth muscle cell growth; myocardial infarction; trauma; cancer; age-related macular degeneration; cytostatic; cardiant; cerebroprotective; ophthalmological; vulnerary. Gerber H, Gerritsen ME, Goddard A; J, Hillan KJ, Marsters SA, Pan J, TK, Williams PM, Wood WI, Ye W; 82; 492pp; English ADH43515 standard; protein; 1124 AA. 26-NOV-2002; 2002US-00305654. 20-JUN-2001; 2001WO-US019692 Godowski PJ, Gurney AL, F 25-MAR-2004 (first entry) Human PRO polypeptide #41 (GETH ) GENENTECH INC 2004-042166/04. Claim 11; SEQ ID NO WPI; 2004-042166/ N-PSDB; ADH43514. US2003224984-A1 04-DEC-2003 ADH43515; Homo RESULT 14 

> 909 99 9 720 720 780 780 840

LINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT LLINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT 1LDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS 1LDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS

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SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR

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841 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 IHRDLAARNILVGENYVAKIADFGLSRGOEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTINSD
 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 AIEYAPHGNILDFIRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 VWSYGVILWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY
 Human; PRO; cardiovascular disorder; endothelial disorder; angiogenic disorder; endothelial cell growth; cardiac hypertrophy; cell apoptosis; cell tube formation; angiogenesis; smooth muscle cell growth; myocardial infarction; trauma; cancer; age-related macular degeneration; cytostatic; cardiant; cerebroprotective; ophthalmological; vulnerary.
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
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 standard; protein; 1124
 98WO-US025108
98WS-00218517.
99WS-00218118.
99US-00214186.
99WO-US005028.
 98WO-US019330.
98WO-US019437.
98US-00180997.
 99US-00267213.
99US-00284291.
99WO-US012252.
99US-00332928.
 99US-00380137.
99US-00380138.
99US-00380139.
 99WO-US020111.
99WO-US020594.
99WO-US020944.
99WO-US021090.
 98WS-00015089.
98WO-US018824.
98WO-US019177.
 99WO-US021547.
99WO-US023089.
99US-00403154.
99US-00403296.
 20-FEB-2002; 2002US-00081056
 20-MAY-2004 (first entry)
 Human PRO polypeptide #41
 US2004043927-A1.
 05-OCT-1999;
15-OCT-1999;
18-OCT-1999;
 Homo sapiens.
 16-SEP-1998
17-SEP-1998
19-NOV-1998
01-DEC-1998
02-DEC-1998
05-JAN-1999
03-MAR-1999
09-MAR-1999
12-ARR-1999
12-ARR-1999
12-ARR-1999
02-JUN-1999
 14-JUN-1999;
14-JUN-1999;
25-AUG-1999;
25-AUG-1999;
01-SEP-1999;
 29-JAN-1998;
10-SEP-1998;
14-SEP-1998;
 08-SEP-1999
 15-SEP-1999
 15-SEP-1999
 04-MAR-2004
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disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma, cancer or age-related macular degeneration. The PRO Polymucleotides are useful as hybridisation probes in chromosome and gene mapping and in generating antisense RNA and DNA, and for chromosome identification and rissue typing. The PRO polypeptides and polymucleotides are also useful in gene therapy and as molecular weight markers for protein electrophoresis purposes. This sequence represents a human PRO
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDARTSLTCIASGWRPHEPITIGRD
 PEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNGVCHEDTGEC
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 MAQA PONVREBPANO PNSGTLALNRKVKNNPDPT IY PVLDWND IK PODVIGEGNFGQVLK
 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL
 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDARTSLTCIASGWRPHEPITIGRD
 FEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRO
 QASFLPATLITATVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 ICPPGFMGRTCBKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
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 LLYKPVNHYBAWQHIQVTNBIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
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 LLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
 LLYKPVNHYBAWQHIQVTNEIVTLNYLBPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 Gaps
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 Length 1124;
 Indels
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 DB
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0; Mismatches
 100.0%;
 polypeptide of the invention.
 Query Match
Best Local Similarity 100.
Matches 1124; Conservative
 Sequence 1124 AA;
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99US-00423741.
99US-00423843.
99WO-US028214.
99WO-US028313.
99WO-US028313.
 99WO-US028564.
99WO-US028565.
99WO-US030995.
99WO-US030999.
 99WO-US031243.
 2000WO-US004414.
 2001WO-US021735.
2001US-00918585.
2001US-00924419.
 2000WO-US000376.
 2000WO-US005601.
 2000WO-US006884,
 2000WO-US007532.
2000WO-US008439.
 2000WO-US013705.
2000WO-US014042.
 2000WO-US020710
 1000WO-US032678
 2001WO-US017092,
2001US-00872035,
 2000WO-US000219
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 2000WO-US023522
 2000WO-US023328
 2000US-00664610
 000US-00665350
 2000WO-US030952
 2000WO-US030873
 2001US-00802706
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 2001US-00828366
 2001US-00866028
 2001US-00866034
 2001WO-US017800
 001US-00882636
 2001WO-US019692
2001WO-US021066
 001US-00931836
 2001US-00941992
 :001US-00946374
 2001US-00002796
 2002US-00053107
99US-00403297
 001US-00948901
 28-FEB-2001; 2
01-MAR-2001; 2
09-MAR-2001; 2
14-MAR-2001; 2
05-APR-2001; 2
 10-NOV-1999;
12-NOV-1999;
22-NOV-1999;
30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
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02-MAR-2000;
10-MAR-2000;
20-MAR-2000;
21-MAR-2000;
31-MAR-2000;
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25-MAY-2001; 2
01-JUN-2001; 2
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13-AUG-2001;
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18-SEP-2000;
08-NOV-2000;
08-NOV-2000;
 19-JUN-2001;
20-JUN-2001;
29-JUN-2001;
 22-MAY-2000;
30-MAY-2000;
 02-JUN-2000;
28-JUL-2000;
 15-JAN-2002;
17-JAN-2002;
 24-FEB-2000;
 17-MAY-2000;
 01-JUN-2001;
14-JUN-2001;
 06-AUG-2001;
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The invention relates to human PRO polypeptides and the PRO polymucleotides encoding them. The invention also relates to treating cardiovascular, endothelial or angiogenic disorders in mammals, inhibiting endothelial or angiogenic disorders in mammals, inhibiting endothelial or angiogenic disorders in properties of the invention or smooth muscle cell growth by administering polypeptides of the invention. The PRO polypeptides and polymucleotides are useful for treating cardiovascular, endothelial or angiogenic disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma, cancer or age-related macular degeneration. The PRO polymucleotides are useful as hybridisation probes in chromosome and gene mapping and in geneting antiennes RNA and DNA, and for chromosome identification and issue typing. The PRO polypeptides and polymucleotides are also useful in gene therapy and as molecular weight markers for protein clectrophoresis purposes. This sequence represents a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
 180
 180
 120
 61 FEALANQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ 120
 240
 240
 300
 300
 360
 360
 420
 9
 9
 Stephan JF;
 New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or PRO21383, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 FEALMNOHOD PLEVTOD VTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRO
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
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 AQPQDAGVYSARY I GGNLFTSAFTR1.I VRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 0; Gaps
 100.0%; Score 6013; DB 8; Length 1124; 100.0%; Pred. No. 0; Anismatches 0; Indels 0;
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Hillan KJ, Marsters SA, Pan J,
1, Wood WI, Ye W;
 Claim 11; SEQ ID NO 82; 494pp; English
 Godowski PJ, Gurney AL, Hillan
Watanabe CK, Williams PM, Wood
 Gerber H,
18-JAN-2002; 2002US-00052594.
08-FEB-2002; 2002US-00072068.
09-APR-2002; 2002US-00119480.
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 (GETH) GENENTECH INC
 WPI; 2004-225727/21.
 Local Similarity
 Sequence 1124 AA;
 N-PSDB; ADK82859.
 Baker KP,
 121 (
 241
 361
 61
 181
 241
 301
 301
 Query Match
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421 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK 480

g δ

Search completed: March 14, 2006, 01:43:41 Job time : 200 secs

"His bade Blauk (nsbto)

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 14, 2006, 01:43:59; Search time 49 Seconds (without alignments) 2207.095 Million cell updates/sec

Title: US-10-633-742-8
Perfect score: 6013
Sequence: I MDSLASLVLCGVSLLLSGTV.....TLYEKFTYAGIDCSAEBAA 1124

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

κο	Description	protein-tyrosine k	protein-tyrosine k					protein-tyrosine k			protein-tyrosine k			fibroblast growth	£	growt				fibroblast growth		fibroblast growth	-		fibroblast growth	fibroblast growth	fibroblast growth	-		fibroblast growth
SUMMARIES	QI QI	I58388	S57846	JN0712	I54237	JH0771	S57845	JN0711	S24066	A35963	A49714	838579	S29840	JH0393	A48991	TVMSFG	TVHU2F	I49289	TVHUFG	TVHUF3	A49120	JC4058	A36477	S19947	B49151	TVCHFG	155363	A56795	S18209	A39752
	03	-	7	Н	7	7	7	Н	Н	~	<b>⊣</b>	~	~	7	~	Н	Н	~	-	Н	~	N	Н	~	~	Н	~	7	~	-
	Length	1124	1125	1123	1122	1125	1136	1134	1138	806	974	797								908	729	818	812	822	822	819	801	729	799	814
	Query Match	100.0	95.3	93.1	95.8	89.3	42.0	41.8	41.8	12.0	11.9	11.9	11.7	11.7	11.6	11.6	11.6	11.6	11.5	11.5	11.5	11.5	11.4	11.4	11.4		11.3	11.3	11.2	11.2
		6013	5732.5	5598.5	5580	5371.5	2526	2515	2511	719.5	717.5	713.5	703.5	701.5	698.5	698.5	696.5	696.5	694.5	693	692	069	989	683	683	682.5	681	678	919	673
	Result No.		7	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

fibroblast growth protein-tyrosine k	fibroblast growth fibroblast growth keratinocyte growt	ilbroblast growth protein-tyrosine k fibroblast growth fibroblast growth	receptor tyrosine fibroblast growth fibroblast growth fibroblast growth fibroblast growth
149293 S57450 JC4583	A49151 JC1450 A38429	B54846 B35963 TVHUF4 S36439	A54846 A57638 S41050 S16236 A45081 S17295
240	1010	00100	หลด [์] ผผน
733 1064 829	816 650 707	8855 8053 8245 8454 8545 8545 8545 8545 8545 8545	1040 1040 748 769 822 820
11.2		10000	
671 671 670	666.5	665.5 662.5 661 661	660.5 659 659 659 659 659
30	1 W W W	0 W W W W	4 4 4 4 4 0 4 6 6 6 6

## ALIGNMENTS

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 Best Local Similarity
Matches 1071; Conservative
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 121
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 Query Match
Best Local (
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 1021 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPINCDDEVYDLMRQCWREKFY 1080
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C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphopt
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A, Cross-references: UNIPARC: UNIPARC: UDIO000136F54; EMBL: X71424; NID: 9296577; PIDN A, Nore: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
R, Sato, T.N.; Qin, Y.; Kozak, C.A.; Andus, K.L.
A, Reference number: S32690
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A, Accession: S32691
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831-839/Kegion: protein kinase ATP-binding motif.
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856,873,965/Active site: Lys, Glu, Asp #status predicted
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 tyrosine kinase
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C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57846; S32691
Proc. Natl. Acad. Sci. U.S.A. 90, 9355-9358, 1993
A;Title: tie-1 and tie-2 define another class of putative receptor tyrosine
A;Reference number: S57845; MUID:94022374; PMID:8415706
A;Accession: S57846
A;Status: preliminary; nucleic acid sequence not shown; translation not show
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 61 FEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRO
 181 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
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 Gaps
 95.3%; Score 5732.5; DB 1; Length 1125; 95.2%; Pred. No. 5.2e-221; Arive 20; Mismatches 33; Indels 1;
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PII

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F;131-137/Product: protein-tyrosine kinase, receptor type tie-2 #status predicted <NAT>
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F;255-298/Domain: EGF homology <EG3>
F;363-340/Domain: EGF homology <EG3>
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F;547-525/Domain: fibronectin type III repeat homology <FN3C>
F;57-110/Domain: tibronectin type III repeat homology <FN3C>
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F;51-10/SDOmain: protein kinase homology <KIN>
F;81-10/SDOmain: protein kinase homology <KIN>
F;82-837/Region: protein kinase homology <KIN>
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R;Dumont, D.J.; Yamaguchi, T.P.; Conlon, R.A.; Rossant, J.; Breitman, M.L.
R;Dumont, D.J.; Yamaguchi, T.P.; Conlon, R.A.; Rossant, J.; Breitman, M.L.
A;Crosser T. 147-1480, 1992
A;Title: tek, a novel tyrosine kinase gene located on mouse chromosome 4, is expressed: A;Reference number: S43494; MUID:92334855; PMID:1630810
 241 ICPPGFMGRICEKACELHIFGRICKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE 300
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 DB 1; Length
 41; Indels
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submitted to the EMBL Data Library, April 1993
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 61
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 protein-tyrosine kinase (EC 2.7.1.112), receptor type tek precursor - mouse NyAlternate names: protein-tyrosine kinase, receptor type tie-2 C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 27-Jun-1994 #text_change 09-Jul-2004 C;Accession: JN0712, S57848; S43459; S43494; S3142 #text_change 09-Jul-2004 C;Accession: JN0712, S57848; S43459; S43494; S3142 #text_change 09-Jul-2004 C;Accession: JN0712, S57848; S43494; S31-399, 1993 Mirayama, A; Hamaguchi, I:; Hashiyama, M; Murayama, Y.; Yasunaga, K.; Suda, T. Biochem Biophys. Res. Commun. 195, 301-399, 1993 A;Tile: Molecular cloning and characterization of mouse TIE and TEK receptor tyrosine k,Accession: JN0712 A;Molecule type: mRNA A;Reference number: JN0711, MUID:93371421; FMID:8395828 A;Residues: 1-1123 <IMA. A;Residues: 1-1123 <IMA. A;Residues: UNIPROT:002858; UNIPARC:UP100001572FB R;Sato, T.N.; Qin, Y.; Kozak, C.A.; Audus, K.L. Proc. Natl. Acad. Sci. U.S.A.; 90, 9355-9358, 1993 A;Title: tie-1 and tie-2 define another class of putative receptor tyrosine kinase genes A;Reference number: S57848; MID:94022374; PMID:8415706
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 genea
 A;Molecule type: mRNA
A;Residues: 1-786,788-1123 <SAT>
A;Cross-references: UNIPARC:UPI000002998B; EMBL:X71426; NID:g296612; PIDN:CAA50557.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
R;Dumont, D.J.
 1019
 1079
 FIHRDIAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLAVSVYTINS 1020
 1080
 840
 80
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 720
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 VWVCSVNTVSGMVEKPFNISVKVLPKPLNAPKVIDTGHNFAVINISSEPYFGDGPIKSKK 480
 not shown
 RMAQAEQNVREEPAVQENSGTLALNRKAKANNPDPTIYPVLDWNDIKFQDVIGEGNFGQVL
 KAR I KKOGLEMDAA I KEMKEYASKODHEDPAGELEVLCKIGHHPNI INLLGACEHRGYLY
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 VLLINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISW
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 RMAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVL
 LAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQXQ
 FIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNS
 IGLPPPRGLNLLPKSQTTLNLTWQPIPPSSEDDFYVEVERRSVQ-KSDQQNIKVPGNLTS
 SSNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQR
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 A; Status: preliminary; nucleic acid sequence not shown; translation
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 1021
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1 MDSLAGLVLCGVSLLLYGVVEGAMDLILINSLPLVSDAETSLTCIASGWHPHEPITIGRD
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 481 LFYKPVN--QAWKYIEVTNEIFTLNYLEPRIDYELCVQLARPGEGGEGHPGFVRRFTTAS
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 FIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNS
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 Gaps
 4 ;
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 92.6%; Pred. No. 6e-215;
ive 37; Mismatches 42;
 Best Local Similarity 92.6%
Matches 1042; Conservative
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 procein-tyrosine kinase (EC 2.7.1.112), receptor type tek precursor - mouse NiAlternate names: protein-tyrosine kinase receptor type tie2
C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: IS4237
C;Accession: IS4237
R;Runting, A.S.; Stacker, S.A.; Wilks, A.F.
Growth Factors 9, 99-105, 1993
A;Title: tie2, a putative protein tyrosine kinase from a new class of cell surface receptation: IS4237; MUD:94031116; PMID:8217221
A;Retrence number: IS4237; MUD:94031116; PMID:8217221
A;Retrence number: IS4237; MUD:94031116; PMID:8217221
A;Retrence number: IS4237; MUD:94031116; PMID:8217221
A;Retrence number: IS4237; MUD:94031116; PMID:9452873; PIDN:AAB28663.1; PID: A;Residues: 1-1122 <RES>
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C;Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology <EG3>
C;Superfamily: protein-type in type III repeat homology <IRM>
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F;321-347,Domain: EGF homology <EG3>
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F;321-1097/Domain: protein kinase homology <IRN>
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 DVWSYGVLLWEIVSLGCTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKP 1079
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 778
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 959
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 999 LAIEYAPHGNLLDFLRKSRVLETDPAFALANSTASTLSSQQLLHFAADVARGMDYLSQKQ
 LAIBYAPHGNILDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQ
 959 FIHRDLAARNILVGENYIAKIADFGLSRGQEVYVKKTMGRLFVRWMAIESLNYSVYTTNS
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 840
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protein-tyrosine kinase (EC 2.7.1.112), receptor type tie precursor - bovine C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Spacession: S57845; S32690
R;Sato, T.N.; Qin, Y.; Kozak, C.A.; Audus K.L.
Proc. Natl. Acad. S2. U.S.A. 90, 3355-3389, 1993
A;Title: tie-1 and tie-2 define another class of putative receptor tyrosine kinase genes A;Reference number: S57845; MUID:94022374; PMID:8415706
A;Accession: S57845
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
A;Status: preliminary; nucleic acid sequence was submitted to the EMBL Data Library, March 1993
A;Crose-references: UNIPROT:Q16805; UNIPARC:UPI0000136F53; EMBL:X71423; NID:9296575; PIDh
A;Crose-references: UNIPROT:Q16805; UNIPARC:UPI0000136F53; EMBL:X71423; NID:9296575; PIDh
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 955 YLSQKQFIHRDLAARNILVGENYIAKIADFGLSRGGEVYVKKTMGRLFVRMMAIESLNYS 1014
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 834 NFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACE
 894 HRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMD
 895 HRGYLYLAIEYAPHGNLLDFLGKSRVLETDPAFCHRQQYSSTLSSQQLLHFAADVARGMD
 954 YLSQKQFIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYS
 KKLLYKPVNHYEAWQH1QVTNE1VTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTT
 ASIGLPPPRGLNLLPKSQTTLNLTWQPI PPSSEDDPYVEVERRSVQ-KSDQQNIKVPGNL
 SWIILDGYSISSITIRYKVQGKNEDQHVDVKIKNAIIIQYQLKGLEPETAYQVDIFAENN
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 1075 CWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCPAEEAA
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 protein-tyrosine kinase (EC 2.7.1.112), receptor type hyk precursor - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 21-Jul-2000
C;Accession: JH0771
R;Norita, X: Yagi, T.; Komura, N; Tomooka, Y; Ikawa, Y; Aizawa, S.
Biochem. Biophys: Res. Commun. 189, 1747-1753, 1992
A;Title: A novel tyrosine kinase, hyk, expressed in murine embryonic stem cells.
A;Reference number: JH0771; MUID:93129253; PMID:1282811
A;Molecule type: mRNA
A;Residues: 1-1125 <HOR>
A;Residues: 1-1125 <HOR>
A;Residues: 1-1125 <HOR>
A;Gene: type: mRNA
A;Gene: hyk
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F;368-00main: fibronectin type III repeat homology <FN3A>
F;368-00main: fibronectin
 F;823-1100/Domain: protein kinase homology «KIN»
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 61 FEALMNQHODPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ 120
 120
 238
 239
 298
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 358
 359
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 300 NEACPSGYYGPDCKLRCHCTNEEICDRFQGCLCSQGWQGLQCEKEGRPRMTPQIEDLPDH
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89.5%; Pred. No. 1.2e-206;
ive 40; Mismatches 66; Indels 13;
 1078 YERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA
 1080 YERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA
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 Query Match
Best Local Similarity 89.5
Matches 1012; Conservative
1018
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 (covalent) #status predicted
 QH--QDPLEVTQDVTREWAKKVVWKR-EKASKINGAYFCEGRVRGEAIRIRTMKWRQQAS 123
 PRPWQPP----HIARNGSSRVTVRGFSQPSDLVGVFSCVG---GGGTRVLYVHNSPGAH 124
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 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC 240
 183 VQPSSSGIYSATYLEASPLGSAFFRLIVRGCEAGRWGQDCTKECPGCLHGGVCHDQDGEC 242
 241 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE 300
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE 360
 361 VNSGKFNPI-CKASGWPLPTNEEMTLVKPDGTV-LHPKDFNHTDHFSVAIFTIHRILPPD 418
 360 FNLDTMPRINCAAAGNPFPVRGSMELRKPDGTVILSTKAIVEPDR-TTAEFEVPRLALGD 418
 SGVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVIN--ISSEPYFGDGPI 476
 475
 KSKKLLYKPVNHYEAWQHIQV-TNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRR 535
 ASVRLHYRPQDSTMAWSTIVVDPSENVTLMALRPKTGYSVRVQLSRPGEGGGGGAMGPPTL 535
 536 FTTASIGLPPPRGLNLLP-----KSQTTLNLTWQ--PI-FPSSEDDFYVEVERRSVQK 585
 SDQQNIKVPGNLTSVLLNNLHPREQYVV------RARVNTKAQGEWSEDLT 630
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 197 NSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKR 856
 16 LSGTVEGAMDLILINSLPLVSDAETSLTCI-----ASGWRPHEPITIGRDFEALMN
 536 MTT----DCPEPL---LKPWLEGWHVEGPDRLRVSWSLPPVPGPLVGDGFLLRLWDGARGO
 LASHVGAAVDLTLLADLRLTEPORFFLTCVSGEAGAGRGSDAWGP--PLLLEKDDRIVRT
 ||:| ||:| |: | |: | || || || || || SGLWECRVSTSGGODSRRFRINVKVPPVPLTAPRLLAKOSRQLVVSPLVS---FSGDGFI
 AWTLSDILPPOPENIKISNITHSSAVISWTILDGYS--ISSITIRYKVQGKNED---QHV
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F;363-426/Domain: immunoglobulin homology <IM2>
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F;540-631/Domain: fibronectin type III repeat homology <FN3B>
F;640-728/Domain: fibronectin type III repeat homology <FN3B>
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F;759-784/Domain: transmembrane #status predicted <TYM>
F;845-112/Domain: protein kinase homology <KIN>
F;843-851/Region: protein kinase ArP-binding motif
F;843-106,370-424/Disulfide bonds: #status predicted
F;84,159,501,594,707/Binding site: carbohydrate (Asn) (covaler F;868,885,977/Active site: Lys, Glu, Asp #status predicted
 73
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A;Accession: S57847
A;Status: preliminary; mucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-598, L', 600-1134 <8A2>
A;Residues: 1-598, L', 600-1134 <8A2>
A;Cross-references: UNIPARC:UPI0000055BBDD; EMBL:X71425; NID:g296610; PIDN:CAA50556.1; PII
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
B;Nothonen, J.; Partanen, J.; Armstrong, E.; Vaahtokari, A.; Elenius, K.; Jalkanen, M.; F
Blod 80, 2548-2555, 1992
A;Ritle: EMbianced expression of the tie receptor tyrosine kinase in endothelial cells du;
A;Reference number: A48926; MUID:93043301; PMID:1384789
 A; Molecule type: mRNA
A; Residues: 1-1134 < IYAA.
A; Cross-references: UNIPROT: Q06806; UNIPARC: UPI0000027C5B; GB:X73960; NID: g402601; PIDN: C
R; Sato, T.N.; Qin, Y.; Kozak, C.A.; Andus, K.L.
submitted to the EMBL Data Library, March 1993
 D.; Alitalo,
 A,Molecule type: mRNA
A,Residues: 1-598, 'L',600-1134 <SAT>
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A,Cross-references: UNIPARC:UDIO00005E8DD; EMBL:X71425; NID:9296610; PIDN:CAA50556.1; PII
R;Sato, T.N.; Qin, Y.; Kozak, C.A.; Audus, K.L.
R;Sato, T.N.; Qin, Y.; Kozak, C.A.; Audus, K.L.
B,Coc., Natl. Acad. Sci. U.S.A. 90, 9355-9358, 1993
A;Title: tie-1 and tie-2 define another class of putative receptor tyrosine kinase genes
A;Reference number: S57845; MUID:94022374; PMID:8415706
 in vivo
 protein-tyrosine kinase (EC 2.7.1.112), receptor type tie precursor - mouse Cispecies: Mus musculus (house mouse)
Cjate: 14-Jul-1994 #sequence revision 14-Jul-1994 #text_change 09-Jul-2004
CjAccession: JN0711; 833141; S57847; A48926; 165403
R;Iwama, A.; Hamaguchi, I.; Hashiyama, M.; Murayama, Y.; Yasunaga, K.; Suda, T.
Biochem. Biophys. Res. Commun. 195, 301-309, 1993
A;Title: Molecular cloning and characterization of mouse TIE and TEK receptor tyrosine. A;Reference number: JN0711; MUID:93371421; PMID:8395828
 A;Status: preliminary; not compared with conceptual translation
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 221-322;740-890 < XOR.
A;Residues: 221-322;740-890 < XOR.
A;Cross-references: UNIPARC:UPI000017260A; UNIPARC:UPI000017260B
A;Note: sequence extracted from NCBI backbone (NCBIP:118660, NCBIP:118662)
A;Note: sequence extracted from NCBI backbone, L.; Janne, J.; Dumont, D.;
Biod 86, 1828-1835, 1995
A;Title: Endothelial-specific gene expression directed by the tie gene promoter:
A;Reference number: 152613; MUID:95383653; PMID:7655012
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 1049
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 916
 989
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 977 VAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGG
 SKIADFGLSRGEEVYVKKTMGRLPVRMAIESLNYSVYTTKSDVWSFGVLLWEIVSLGG
 1050 TPYCGMTCAELYEKLPQAYRMEQPRNCDDEVYELMRQCWRDRPYERPFRQIALQLGRML
 SRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENY
 1037 TPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRML
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
 EERKTYVNTTLYEKFTYAGIDCSAEEA 1123
 A; Reference number: S32690
 Accession: I65403
 A; Accession: JN0711
 A; Accession: S33141
 1097
 917
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Z

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A; Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C; Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin type
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphot
 A; Cross-references: GDB:212873; OMIM:600222
 A;Molecule type: mRNA
A;Residues: 981-1034 < PAW>
A;Cross-references: UNIPARC:UP10000172609
A;Experimental source: clone JTK14
 A;Status: translated from GB/EMBL/DDBJ
 A; Map position: 1p34-1p33
 A; Gene: GDB:TIE; JTK14
 A;Residues: 1-19 <RES>
 A; Molecule type: DNA
 Accession: I52613
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 Genetics:
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A;Cross-references: UNIPARC:UPI000017260C; GB:S79346; NID:g1086920
C;Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology, fibronectin type; Keywords: AFF, autophosphortlation; duplication; glycoprotein; phosphoprotein; phosphof F;1-21/Domain: signal sequence #status predicted <SIG>F;22-1134/Product: protein-tyrosine kinase, receptor type tie #status predicted <MAT>F;26-105/Domain: EGF homology <EGI>F;25-300/Domain: EGF homology <EGI>F;25-300/Domain: EGF homology <EGI>F;304-342/Domain: EGF homology <EGI>F;304-342/Domain: immunoglobulin homology <IM2>F;304-362/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2>F;305-365/Domain: immunoglobulin homology <IM2F;305-365/Domain: immunoglobulin homology <IM2F;305-365/Domain: immunoglobulin homology <IM2F;305-365/Domain: immunoglobulin homology <IM2F;305-365/Domain: im
 (covalent) #status predicted
 24;
 347 RMTPKIVDLPDHIEVNSGKFNPI-CKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFS 405
 347 -RIPQILSMATEVĖFNIGTMPRINCAAAGNPFPVRGSMKLRKPDGTMLLSTKVIVEPDRT 405
 406 TAEFEVPSLILGDSGFWECRVSTSGGDSRRFKVNVKVPPVPLTAPRLLAKQSRQLVVSP 465
 522
 574
 -----VNT 619
 620 KAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILDGYS--ISSITIRYKVQ 677
 ------FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVR 107
 64 DRIVRIFPPGQPLYLARNGSHQVTLR-------GFSKPSDLVGVFSCVGGAG 108
 108 GEAIRIRTMKMRQQASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPR 167
 CMNNGVCHEDTGECI CPPGFMGRTCEKACELHTFGRTCKGRCSGQEGCKSYVFCLPDPYG 286
 CSCATGWKGLQCNEACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIP 346
 106 VAIFTIHRILPPDSGVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVIN- 464
 465 -ISSEPYFGDGPIKSKKLLYKPVNHYEAWQHIQV-TNEIVTLNYLEPRTEYELCVQLVRR 522
 -------PPAPRHLHAQALSDSBIQLMWQHPEAPSGPISKYIVEIQVA 680
 -----NNIG 719
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 63
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SSLLL--PTLFLASHVGASVDLTLLANLRITDPQRFFLTCVSGEAGAGRSDPPLLLEKD
 HEVPD-ILEVHLPHAQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTA
 GEGGEGHPGPVRRFTTASIGLPPPRGLNLLP-----KSQTTLNLTWQ-PIFPSSEDDF
 5 ASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIA----SGWRPHEPITIGRD
 Query Match
41.8%; Score 2515; DB 1; Length 1134;
Best Local Similarity 45.6%; Pred. No. 4.5e-93;
Matches 540; Conservative 159; Mismatches 364; Indels 122
 <FN3B>
 678 GKNED-QHVDVKIKNATIIQYQLKGLEPETAYQVDIFAE------
 F,47-28/Domain: fibronectin type III repeat homology cFN3 F;540-629/Domain: fibronectin type III repeat homology cFN3 F;540-629/Domain: fibronectin type III repeat homology cFN3 F;57-782/Domain: fibronectin type III repeat homology cFN3 F;57-782/Domain: protein kinase homology cKIN> F;841-849/Region: protein kinase homology cKIN> F;841-849/Region: protein kinase ATP-binding motif F;841-849/Region: protein kinase ATP-binding motif F;811-89,501,592,705/Binding site: carbohydrate (Asn) (cova F;865,883,975/Active site: Lys, Glu, Asp #status predicted
 575 YVEVERRSVOKSDOQNIKVPGNLTSVLLNNLHPREQYVVRAR-
 61
 523
 287
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protein-tyrosine kinase (EC 2.7.1.112), receptor type tie precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S24066; C38269; I52613
R;Partanen, J.; Armstrong, E.; Maekelae, T.P.; Korhonen, J.; Sandberg, M.; Renkonen, R.; Mol. Cell. Biol. 12, 1698-1707, 1992
A;Title: A novel endothelial cell surface receptor tyrosine kinase with extracellular epi A;Reference number: S24066; MuID:92195316; PMID:1312667
 R; Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K. Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: C38269
A;Accession: C38269
 R;Korhonen, J.; Lahtinen, I.; Halmekyto, M.; Alhonen, L.; Janne, J.; Dumont, D.; Alitalo, Blood 86, 1828-1835, 1995
A;Title: Endothelial-specific gene expression directed by the tie gene promoter in vivo. A;Reference number: 152613; MUID:95383653; PMID:7655012
 PID:
 A;Cross-references: UNIPARC:UP1000000503; GB:S79347; NID:g1086921; PIDN:AAD14299.1;
 959 OFIHRDLAARNIIVGENYVAKIADFGLSRGOEVYVKKTMGRLPVRWMAIESLNYSVYTTN 1018
 1019 SDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREK 1078
 958
 738
 779
 789
 838
 849
 898
 909
YLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQK
 970 QFIHRDLAARNVLVGENLASKIADFGLSRGEEVYVKKTWGRLPVRWMAIESLNYSVYTTK
 LKAR I KKDGLRMDAA I KRMKEYASKDDHRDFAGELEVLCKLGHHPN I INLLGACEHRGYL
 720 SSNPAFSHELVTLPESQAPADLGGGKWLLIAILGSAGMTCLTVLLAFLIILQLKRANVQR
 RMAQAFQN-VREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQV
 1079 PYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEA 1123
 A;Molecule type: mRNA
A;Residues: 1-1138 <PAR>
A;Cross-references: UNIPARC:UP1000002CA84; EMBL:X60957
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Signer cek2
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei C; Superfamily: hTP autophosphorylation; duplication; glycoprotein; growth factor receptor; F; 1-23/Domain: signal sequence #status predicted <SIG>F; 24-806/Product: protein-tyrosine kinase cek2 #status predicted <MAT>F; 24-369/Domain: extracellular #status predicted <EXT>F; 24-369/Domain: immunoglobulin homology <IMM>F; 26-355/Domain: immunoglobulin homology <IMM>F; 26-355/Domain: immunoglobulin predicted <IMM>F; 369-369/Domain: intracellular #status predicted <IMT>F; 390-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INT>F; 300-806/Domain: intracellular #status predicted <INTO *INT>F; 300-806/Domain: intracellular #status predicted <INTO *INT>F; 300-806/Domain: intracellular #status predicted <INTO *INT>F; 300-806/Domain: intracellular #status predicted <INTO *INT>F; 300-806/Domain: intracellular #status predicted <INTO *INT>F; 300-
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A;Residues: 1-806 <PAS>
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 F;464-749/Domain: protein kinase homology <KIN>
F;472-480/Region: protein kinase Arp-binding motif
F;472-480/Region: protein kinase Arp-binding motif
F;61-107,170-222,269-333/Disulfide bonds: #status predicted
F;96,219,256,288,309,322/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;602,519,511/Active site: Lya, Gilu, Asp #status predicted
F;642/Binding site: magnesium (Asn, Asp) #status predicted
F;642/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 SRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCA 1045
 ELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNT 1105
 925
 940
 985
 DGIGIAPS--NRT-HIGOKLLKIINVSYDDSGLYSCKPRHSNEVLG-----NFTVRVTD 125
 KPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKKLLYKPVNHYEAWQHIQVTNEIVTLN 505
 F, Pasquale, E.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 5812-5816, 1990
A, Title: A distinctive family of embryonic protein-tyrosine kinase receptors. A, Reference number: A35963, MUID:90332672; PMID:2165604
A, Rocession: A55963
A, Status: preliminary
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 PAIANSTASTLSSOQLLHFAADVARGMDYLSOKOFIHRDLAARNILVGENYVAKIADFGL
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 KVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDD
 HRDFAGELEVLCKLGHHPNI INLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPA
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 precursor
 cek2
 protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-1990 #sequence_revision
 SLFENFTYAGIDATAEEA 1138
 TLYEKFTYAGIDCSAEEA 1123
 Accession: A35963
 1046
 1001
 1106
 1121
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 Fig. 2-1138/Product: protein-tyrosine kinase, receptor-type tie #status predicted Fig. 2-1138/Product: protein-tyrosine kinase, receptor-type tie #status predicted Fig. 25-1138/Product: protein-tyrosine kinase, receptor-type tie #status predicted Fig. 25-1138/Product: protein-tyrosine kinase, receptor-type tie #status predicted Fig. 25-100/Domain: EGF homology Fig. 25-302/Domain: EGF homology Fig. 25-434/Domain: EGF homology Fig. 25-430/Domain: Edpronectin type III repeat homology Fig. 230/Domain: fibronectin type III repeat homology Fig. 230/Domain: fibronectin type III repeat homology Fig. 231/Domain: fibronectin type III repeat homology Fig. 231/Domain: fibronectin type III repeat homology Fig. 231/Domain: protein kinase homology Fig. 37-114/Domain: protein kinase ATP-binding motif
Fig. 37-1114/Domain: protein kinase ATP-binding motif
Fig. 331-105, 332-426/Disulfide bonds: #status predicted (Asn) (covalent) #status predicted Fig. 331, 501, 503, 596, 709/Banding site: carbohydrate (Asn) (covalent) #status predicted Fig. 370, 596, 709/Active site: Lys, Glu, Asp #status predicted
 65 MNQHQDPLEVTQDVTREWAKKVVWKR-EKASKINGAYFCEGRVRGEAIRIRTMKMRQQAS 123
 | | : : | : : | : : | | RTPPGPPLR----LARNGSHQVTLRGFSKPSDLVGVFSCVGGAGARRTRVIYVHNSPGAH 126
 FLPATLIMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPD---ILEVHLPH 180
 127 LLPDKVTHTVNKGDTAVLSARVHKEKQTDVIMKSNGSYFYTLDWHEAQDGRFLLQ--LPN 184
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC 240
 241 ICPPGFMGRICEKACELHTFGRICKERCSGQEGCKSYVPCLPDPYGCSCATGWKGLQCNE 300
 301 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCERGIPRMTPKIVDLPDHIE 360
 VNSGKFNPI-CKASGWPLPINEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDS 419
 FNLETMPRINCAAAGNPFPVRGSIELRKPDGTVLLSTKAIVEPEKTTAEFEVPRLVLADS 421
 GVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVIN--ISSEPYFGDGPIK 477
 SKKLLYKPVNHYEAWQHIQV-TNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRF 536
 TTASIGLPPPRGLNLLP-----KSQTTLNLTWQ-PIFPSS--EDDFYVEVERSVQKS 586
 593 RRENVSSPOARTA-LLTGLTPGTHYOLDVQLYHCTLLGPASPPAHV-LLPPSGPPAPRHL 650
 646 KISNITHSSAVISW---TILDGYSISSITIRYKVQGKNEDQ---HVDVKIKNATIIQYQL 699
 KGLEPETAYOVDIFA-----ENNIGSSNPAFSHELVTLPESOAPADLGGGKM 746
 | |: | |: || |: || |: :| | |: :| | |: :| | | |: :| | | |: :| | |: :| | |: :| | |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :|
 14 LLLSGTVEGAMDLILINSLPLVSDAETSLTCI-----ASGWRPHEPITIGRDFEAL
 HAQALSDSEIQLTWKHPEALPG-PISKYVVEVQVAGGAGDPLWIDVDRPEETSTII----
 DQQNIKVPGNLTSVLLNNLHPREQYVVRARV-NTKAQGEWSEDLTAWTLSDILPPQPENI
 80;
 Length 1138;
 41.8%; Score 2511; DB 1; Length 1 ilarity 46.5%; Pred. No. 6.6e-93; Conservative 165; Mismatches 374; Indels
F;1-21/Domain: signal sequence #status predicted <SIG>
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 al Similarity
539; Conservat
 Query Match
Best Local S
Matches 539
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 181
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44 IARPLWAKHHRPKRGLTSGRWPPQGAK-PSATSVGQLKFNPTVGHVVINELKDVTFNCSI 102
 314 -AVPOSNVSLLLFNTSVPPHVYRIQQLWPMADYNI--SVSCKNEVGWSAFSPWITASTTE 370
 103 KVPQLLVRPDSPGISLWKDGRELHTLDRIATSHFEILDEEEVAMTSTFSIRAAQRSDNGS
 532 PVRRFTTASIGLP-PPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQN
 267 QVN-----VXGIPSAPKAVHVLKRMAHSIVISWVPGF-----DAFSALNSCSVQVKE---
 591 IKVPGNLTSVLLNN-----LHPREQYVVRARVNTKAQGEWSED---LTAWTLS
 636 DILPPQPENIKIS-NITHSSAVISWT-----ILDGYSISSITIRYKVQGKNEDQHV
 686 DVKIK-NATIIQYQLKGLEPETAYQVDIFAENNIGS-SNPAF----SHELVTLPESQAPA
 740 DIGGGKMILIAILGSAGWICLIVILIAFLIILO--LKRANVORRMAQAFONVREE----
 S-GNTDSFIVAL----GFVCGTVAVGLILCLSVVIQKRCMETKYGNAFSRNDSELVVNYT
 -----PAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIK
 845 K-DGLRMDAAIKRMKEYASKDDHRDFAGEL-EVLC-KLGHHPNIINLLGACEHRGYLYLA
 598 OPECTPOKVÁVKTMK--LDNFSHREIEEFLSBAACMKDFDHPNVÍKLLGVC----IELS
 MDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSR----GQEVYVKKTMGRLPVRWMAIE
 330 LCSPGWQGLQCEREGIP--RMTPKIVDLPDHIEVNSGKFNPI------CKASGWPLPT
 380 NEEMTLVKP-----AGTVLHPKDFNHTDHFSV------AIFTIHRILPPDSGV
 WVCSVNTVAG--MVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSK
 480 KLLYKPVNHYEAWQHIQVTNEIVTLNYLEPR-----TEYELCVQLVRRGEG-GEGHPG
 371 GAPTTQPLNVTVSLNESSSFLEIRWVKPPLERTHGELQGYH-----IWHTWQDSKGLQNI
 902 IEYAP-----HGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARG
Best Local Similarity 28.0%; Pred. No. 1.2e-21;
Matches 249; Conservative 141; Mismatches 328; Indels 172;
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 FGLSR----GQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPY 1039
 1040 CGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEER 1099
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 629
 LDGYSISSITIRYKVQGKN-EDQHVDV-KIKNAŢIIQYQLKGLEPETAYQVDIFAENNIG 719
 L------EDAGEYTCLAGNSIG 340
 811
SPSSGDDEDDDDES----EDTGVPFWTRPDKMEKKLLAVPAANTVRFRCPAGGNPTPTIY 181
 : | | ::: | | | ::: | | 396 KKAMNTTTVQKVSKFPLKRQQVSLBSNSSMNSNTPLVRITRLSSSDGPMLANVSBLELPP
 |-----KWELARSRLTLGKPLGEGCFGQVVMAEAIGIDKDKPNKAITVAVKMLKDDAT
 566 IFPSSEDDFYVEVERR-----SVQKSDQQNI---KVPGNLTSVLLNNL----
 ----HPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTI
 ---TLALNRKVKNNP
 DPTIYPVLDW----NDIKFQDVIGEGNFGQVLKAR---IKKD--GLRMDAAIKRMKEYAS
 863 KDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLET
 YLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTASIGLPPPRGLNLLPKSQTTLNLTWQP
 VT-----
 720 SSNPAFSHE---LVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRAN
 DPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIAD
 272 YSDAQPHIQWLKHVEVNGSKYG---PDGTPYV----
 KT--YVNTTL-YEKFTYAGID----CSA 1120
 STDEYLDLSVPFEQYSPAGQDTHSTCSS 777
 777 VQRRMAQAFQNV----REEPAVQFNSG---
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A;Status: preliminary
A;Molecule type: mRNA
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A;Molecule type: mLNA
A;Cross-references: universor; universor; proper
C;Superfamily: Tyrosine-protein, kinase, receptor proto-oncogene AXL type; fibronectin ty
C;Superfamily: Tyrosine-protein typespecial typespecial
B;201-254/Domain: immunoglobulin homology <ml>KINN>
E;575-851/Domain: protein kinase homology <ml>KINN>
E;583-591/Region: protein kinase ATP-binding motif
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C;Species: IO-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A49714
R;Jia, R.; Hanafusa, H.
J. Biol. Chem. 269, 1839-1844, 1994
A;Title: The proto-oncogene of v-eyk (v-ryk) is a novel receptor-type protein tyrosine A;Reference number: A49714; MUID:94124527; PMID:7507487
protein-tyrosine kinase (EC 2.7.1.112) c-eyk precursor - chicken
 A; Accession: A49714
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11.9%; Score 717.5; DB 1; Length 974;

Query Match

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DIMSSCWRAEPADRPTFSQLKVHLEKILESLPAPRGSKDVIYVNTSLPEE 870 RESULT 11

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1009 SINYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVY 761 SLADRVYTTKSDVWARGVTWWREIATRGWTPYPGVQNHEIYEYLFHGQRLKKRENCLDELY

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A;Residues: 1-822 <YAZ>
A;Cross-references: UNIPROT: Q04589; UNIPARC: UPI000012A727; EMBL: D12498; NID: 9220737; PIDN A;Cross-references: UNIPROT: Q04589; UNIPARC: UPIDNOSDIO 1; immunoglobulin homology; protei C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei F;171-232 (Domain: immunoglobulin homology <IMM's F;7476-761/Domain: protein Kinase homology <IMM's F;7476-761/Domain: protein Kinase homology <IMM's F;448-492/Region: protein kinase AIP-binding motif
 rat tissues
 28;
 383
 802
 384 AFLISCMVGSVIIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLL 443
 849
 561
 962
 -----DGTVL,HPKDFNHTDHFSVAIFTIHRILPPDSGVW 422
 ACVINSPSGSDTIYFSVNVSDALPSSEDDDDDDS-----SSEEKETDNIKPNR-- 148
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 327 HLRNVSFEDAGEYTCLAGNSIGLSHHSAMLTVLEALEERPA---VMTSPLYLEIIIYCTG 383
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 301
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 -----NTIDKEMEV-----L 326
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 66
 C'Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_cnange oy-uur-zoov. C'Accession: S29840
E;Accession: S29840
E;Vazaki, N.; Fujita, H.; Ohta, M.; Kawasaki, T.; Itoh, N.
Biochim: Biophys. Acta 1172, 37-42, 1993
B;Title: The structure and expression of the FGF receptor-1 mRNA isoforms in A;Reference number: S29840; MUID:93176824; PMID:8382532
 GWRGLLFWAVLVTATLCTARPAP-----TLPE-------QAQPWGVPVEVES 42
 ibroblast growth factor receptor 1 - rat
;Species: Rattus norvegicus (Norway rat)
;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 MTCLIVLLAFLIILQL----KRANVQRRMA------QAFQNVREEPAVQFNSGTLA
 EYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIH
 LN-RKVKNNPDPTIYPVLDW---NDIKFQ-----DVIGEGNFGQVLKARIKXDGLR
 334 GWOGL------OCEREGIPRMTPKIVDLPDHIEVNSGKFNPICKASGWPLPTNEEM
 43 LLVHPGDLLQLRCRLRDDVQSINWLRDGVQL--AESNRT-RITGEEVEVRDSIPADSGLY
 | : | : | : | 106 EFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRP
 QLKGLEPETAYQVD1FAENNIG-SSNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAG
 482 LYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTASI
 LPPQPENIKISNITHSSAVISWTILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQY
 GLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDF--YVEVERRSVQKSDQQNI-----
 ----KVPGNLTSVLLNNL------HPREQYVVRARVNTKAQGEWSEDLTAWTLSDI
 Gaps
 Indels 197;
 Length 822;
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 384 TLVKP-----
 A;Status: preliminary
 A; Molecule type: mRNA
 A; Accession: S29840
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 A;Cross-references: UNIPROT:Q91287; UNIPARC:UP10000175635; EMBL:X75603
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Superfamily: prowth factor receptor receptor 1; immunoglobulin homology; prote
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F;456-741/Domain: protein kinase homology <KIN>
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 28;
 455
 389 DGTVLHPKDFNHTDHFSVAIFTIHRILPPDSGVWVCSVNTVAGMVEKPFNISVKVLPKPL 448
 NAPNVIDTGHNFAVINISSEPYFGDGPIKSKKLLYKPVNHYEAWQHIQVTNEIVTLNYLE 508
 K----AQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILDGYSISSITIRYK 675
 240 PHRPILQAGFRSNKTVVVGSDV-----EFHCKVYSDAQPHIQW------LKHVEVNGS 286
 727
 287 KFGPDGNPYVTV-LKTAGVNTSDKELEIQF-LRNVTFEDAGEYTCLAGNSIG----YSH 339
 HSAWLTVLPPAEPVPDVDTS----VSILAAAGCVAVVILVVIIIFTYKMKMPSKKTMNTA 395
 NDIKFQDVIGEGNFGQVLKA---RIKKD--GLRMDAAIKRMKEYASKDDHRDFAGELEVL 876
 CKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTL 936
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 71 DGISVDPPTWSHTGQ---KLLKIINVSYDDSGVYSCKARQSSEVLR---NVTVRVTDSPS 124
 E---LVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQA 784
 F-----QNVREEPAVQFNSGT-LALNRKVKNNPDPTIYPV------LDW 821
 SSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSR---GQEVYV 993
 180 KNGKEFKGEHRIGGIKLRHOOWSLVMESVVPSDRGNYTCVVANKYGTIRETYTLDVLERT
 676 VQGKNEDQHVDVKIKNATI-----IQYQLKGLEPETAYQVDIFAENNIGSSNPAFSH
 TVHKVSKFPLKRQVSLESNSSMNSNTPLVRITRLSSSDGPMLANVSELELPADPKWELSR
 SELTLGKPLGEGCFGQVVMADAVGIEKDKPNKATSVAVKMLKDDATDKDLSDLVSEMEMM
 -----AANTV-----
 PRIEYELCVQLVRRGEGGEGHPGPVRRFTTASIGLPPPRGLNLLPKSQTTLNLTWQPIFP
 -----SITWL----SPRCPAAGKPTP-----SITWL---
 SSEDDFYVE-----VERRSVQKSDQONIKVP---GNLTSVLLNNLHP-REQYVVRARVNT
 Gaps
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 SCDDEDDDEES----ESANAPKFTRPEWMEKKLLAVP---
 1111 FTYAGID----CSA 1120
 YSPACPDSHSSCSS 769
A;Reference number: S38579
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A,Molecule type: mRNA
A,Residues: 1-797 <SHI>
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 125
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 322
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 Query Match
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Page 11

Qy 963 RDLAARNILVGENYVAKIADFGLSRGQEVYVKKIMGRLPVRWMAIBSLNYSVYTINS 1019	Qy 732 LPESQAPADLGGGKMLLIAILGSAGWTCLTVLLAFLIILQLKRANVQRRWA 782
OY 1020 DVWSYGVLAWEIVSLGGTPYCGWTCAELYEKLPQGYRLEKPLNCDDEVYDLARROCWREKP 1079	Qy 783QAFQNVREEPAVQFNSCTLALN-RKYKNNPDPTIYPVLDWNDIKFQ 827 :         : : :     :     :: Db 429 KSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPWLAGVSRYELFEDPRWELPRDRL 488
QY 1080 YERPSFAQILVSLARMLEERKTYVATTL 1107  :             :	QY 828DVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLC 877 :
RESULT 13	878 KLGHPNIINLLGACEHRGYLYLAIBYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLS
JH0393 fibroblast growth factor receptor precursor - mouse	Db 547
N;Contains: protein-tyrobins xinade (EC 2.7.1.112) C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999	OY 938 SQUILIFFANDYRENDISCROFTHROLINGERIVAR THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERAL THE GENERA
C:Accession: JH0393 R;Kouhara, H.; Kasayama, S.; Saito, H.; Matsumoto, K.; Sato, B. Bjochem. Biophys. Res. Commun. 176, 31-37, 1991 A:Yitle: Expression cDNA cloning of fibroblast growth factor (PGF) receptor in mouse bre	Qy 995 KTMGRLPVRMMAIESLNYSVYTTNSDVMSYGVLLMEIVSLGGTPYCGMTCAELYBKLPQG 1054
A; Reference number: JH0393; MUID:91207411; PMID:1708247 A; Accession: JH0393	Oy 1055
A;Molecule 1-ype: mrava A;Mosidues: 1-832 (KOU)- A;Cross-references: UNIPARC:UPI000016CD52; GB:M65053; NID:g193292; PIDN:AAA37620.1; PID:	Db 727 HRMDKPSNCTNELYNMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSI 781
A.Experimental source: breast cancer cell line SC-3 A.Morte: the authors translated the codon ATG for residue 397 as Ile and CTG for residue C.Superfamily: basic fibroblast crowth factor receptor 1: immunoslobulin homology, prote	RESULT 14 A48931
C; Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor; F:1-21/Domain: signal sequence #status predicted <sig></sig>	heparin-binding growth factor receptor - mouse Nighternate names: HBGF receptor Nighternate names: HBGF receptor (FC 2 7 1 112)
<pre>Fi2Z-832/Froduct: IlDroblast growth factor receptor #status predicted <for>Fi3Z-922/Domain: immunoglobulin homology <imm> Fi3S-409/Domain: transmembrane #status predicted <imm></imm></imm></for></pre>	N;Concains: piocein-vyloaine Ainase (bc. 2./.i.iis) N;Cobcies: Neus musculus (house mouse) C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
F.486-711/Domain: protein kinase homology <kin> F.494-502/Region: protein kinase ATP-binding motif</kin>	C;Accession: A48991 R;Katoh, O.; Hattori, Y.; Sasaki, H.; Sakamoto, H.; Fujimoto, K.; Fujii, T.; Sugimura, T.
F;67-113,188-240,287-351/Disulfide bonds: #status predicted F;524,541,633/Active site: Lys, Glu, Asp #status predicted	Cancer Res. 53, 1136-1141, 1993 AjrItle: Isolation of the complementary DNA encoding a mouse heparin-binding growth facton a before number, a48891, MITD:9417764; PMID:8487556
Query Match 11.7%; Score 701.5; DB 2; Length 832; Best Local Similarity 26.9%; Pred. No. 4.3e-21; Matches 225; Conservative 133; Mismatches 282; Indels 195; Gaps 25;	A;Accession: A4891 A;Status: preliminary A;Molecule type: nucleic acid
372 ASGWPLPINEMTLVKPDGTVLHPKDFNHTDHFSVAIFT 410	A;Residues: 1-800 <kat> A;Cross-references: NID:g298329; PIDN:f A;Cross-references: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nrsin: Nr</kat>
Db 43 AQPWGVEVEVESLLVHPGDLLQLRCRLRDDVQSINWLRDGVQLVESNRT-RITGEEVE 99	Ajaxperimental Bource: Drain AjNote: sequence extracted from NCBI backbone (NCBIN:126536, NCBIP:126537) C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
QY 411 IHRILPPDSGVWVCSVNTVAGMVEKPFNISVK-VLPKPLNAPNVIDTGHNFAVINISSE- 468   :           ::	C;Keywords: ATP; growth factor receptor; heparin binding; phosphotransferase; tyrosine-sp F;262-335/Domain: immunoglobulin homology «IMM» F;464-749/Domain: protein Kinase homology «KIN» F-473-480/Region: protein kinase ATP-binding motif
QY 469PYFGDGPIKSKKLLYKPVNHYBAWQHIQVTNBIVTLNYLEPRTBYELC 516	Query Match 11.6%; Score 698.5; DB 2; Length 800; Best Local Similarity 28.6%; Pred. No. 5.5e-21; 147; Can 26.
Qy 517 VQLVRRGEGGEGHPGPVRRFTTASIGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDF 574	388 PDGTVLHPKDFNHTDHFSVALFTIHRILPPDSGVWVCSVNTVAGMVEK 4
575 YVEVERRSVQKSDQQNIKVPGNLTSVLLNNLHPREQYY	66 PTGPTVWAKDGTGLVASHRILVGPQRLQVLNASHEDAGVYSCQHRLTRRVL
241 IVENEYGSINHTYQLDVVERSPHRPHPSAGLPANKTVALGSNVEFMCKVYSDPQPHIQWL	OY 436 PFNISYKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKKLLYKEVNHYEAWQH1 495
Qy 613 VRAR\NTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILDGYSISITI 672	QY 496 QVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTASIGLPPPRGLNLLPKS 555
Oy 673 RYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIG-SSNPAFSHELVT 731	Qy 556 QTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSVLLMNL 605 :       : :       : :   Db 217 RGNYTCVVENKFGSIRQTYTLDVLERSPHRPILQ-AGLPANQTAILGSDVEFHCKVYSDA 275

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A; Molecule type: mRNA
A; Residues: 1-30,120-228, 'S',230-255, 'ILQ',259-269,'A',271-543,'M',545-755,'R',757-764,'I
A; Cross-references: UNIPARC: UP1000016CD53; GB: M33760; NID: g193298; PIDN: AAA37622.1; PID: SR; Harada, T.; Saito, H.; Kouhara, H.; Kurebayashi, S.; Kasayama, S.; Terakawa, N.; Kishin Biochem. Biophys. Res. Commun. 205, 1057-1063, 1994
A; Tille: Murine fibroblast growth factor receptor 1 gene generates multiple messenger RN; A; Reference number: PC2277; MUID: 95100926; PMID: 7802632
 A, Molecule type: DNA
A, Residues: 1-15 cHAR2.
A, Residues: 1-15 cHAR2.
A, Cross-references: UNIPARC: UPI0000170CA4; GB:S74765; NID:G833887; PIDN:AAB32845.1; PID:C
C, Comment: This protein mediates the biological actions of heparin-binding growth factors
C, Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protesi
C; Reywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; grotein, glycoprotein; grotein
 Filt-232/Domain: immunoglobulin homology <IMM>
Fi37-397/Domain: immunoglobulin homology <IMM>
Fi37-397/Domain: transmembrane #status predicted <IMM>
Fi38-822/Domain: intracellular #status predicted <INT>
Fi48-492/Romain: protein kinase APP-binding motif
Fi484-492/Rogion: protein kinase APP-binding motif
Fi55-101,178-230,277-341/Disulfide bonds: #status predicted
Fi55-101,277,240,264,296,317,330/Binding site: carbohydrate (Asn) (covalent) #status predicted
Fi514,531,623/Active site: Lys, Glu, Asp #status predicted
Fi628,641/Binding site: magnesium (Asn, Asp) #status predicted
Fi658/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predictec
 ,1-21/Domain: signal sequence #status predicted <51G>
2-822/Product: fibroblast growth factor receptor 1 #status predicted <MAT>
2-822/Product: fibroblast growth factor seceptor 1 #status predicted <5XX>
2-30,120-822/Product: fibroblast growth factor receptor 1, short form #status predicte
 A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-30,120-228,'S',230-255,'ILQ',259-269,'A',271-543,'M',545-628,'LV',631-755,'
A;Cross-references: UNIPARC:UP100001725FD; GB:M33760
(FGF) receptor expressed in CHO cells is PMID:2161540
 243 YQLDVVERSPHRPHPSAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG- 301
 323 MEV-----LHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPA---VWT 370
 -----NTTDKE 322
 VDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIG-SSNPAFSHELVTLPESQAPADLGG 743
 87 EVRDSIPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSEDDDDDDDS-----SSE
 529 HPGPVRRFTTASIGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDF--YVEVERRSVQKS
 PYFGDGPIKSKKLLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEG
 587 DQQNI------KVPGNLTSVLLNNL------HPREQYVVRARVNTKAQGE
 30 QAQPWGVPVEVESLLVHPGDLLQLRCRLRDDVQSINWLRDGVQL--VESNRT-RITGEEV
 10 TIHRILPPDSGVWVCSVNTVAGMVEKPFNISVK-VLPKPLNAPNVIDTGHNFAVINISSE
 625 WSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILDGYSISSITIRYKVQGKNEDQH
 Gaps
 Query Match 11.6%; Score 698.5; DB 1; Length 822; Best Local Similarity 27.1%; Pred. No. 5.6e-21; Matches 223; Conservative 139; Mismatches 294; Indels 167;
 'Title: A murine fibroblast growth factor 'Reference number: A35794; MUID:90272715;
 R;Basilico, C.
Submitted to GenBank, March 1990
A;Reference number: A43025
A;Accession: A43025
 F;126-133/Region: acidic
 A; Accession: A35794
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 A;Residues: 1-147,1150-255,'ILQ',259-439,'A',441-755,'R',757-822 <SAF>
A;Cross-references: UNIPARC:UPI000016CD4D; EMBL:X51893; NID:950959; PIDN:CAA36175.1; PIE
R;Mansukhani, A.; Moscatelli, D.; Talarico, D.; Levytska, V.; Basilico, C.
Proc. Natl. Acad. Sci. U.S.A. 87, 4378-4382, 1990
 A,MOJECCULE type: mRNA
A,Residues: 1-30,120-822 < RE2>
A,Residues: 1-30,120-822 < RE2>
A;Cross-references: UNIPARC:UPI00001725FC; GB:M28998
A,Note: the shorter form is expressed at higher levels in neuronal cells at early stages
R,Safran, A.; Avivi, A.; Orr-Urtereger, A.; Neufeld, G.; Lonai, P.; Givol, D.; Yarden, Y
A,Title: The murine flg gene encodes a receptor for fibroblast growth factor.
A,Reference number: S09953; MUID:90265603; PMID:2161096
 expresse
 A,Molecule type; mRNA
X,Rebidues: 1-822 <REI>
A;Cross-references: UNIPROT:P16092; UNIPARC:UP10000161D54; GB:M28998; NID:g192164; PIDN:
A;Accession: B34849
 fibroblast growth factor receptor 1 precursor - mouse
NyAlternate names: basic fibroblast growth factor receptor
NyAlternate names: basic fibroblast growth factor receptor
NyContains: protein-tyrosine kinase (EC 2.7.1.112) f1g
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C;Accession: A34849; Bay4849; B34849; B35794; A43025; PC2277
R;Reid, H.H.; Wilks, A.F.; Bernard, O
Proc. Natl. Acad. Sci. U.S.A. 87, 1596-1600, 1990
A;Title: Two forms of the basic fibroblast growth factor receptor-like mRNA are of A;Reference number: A34849; MUID:90160373; PMID:1689490
 EVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYE 1049
 1050 KLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKT--YVNTTL 1107
 566 SISSITIRYKVQGKN-EDQHVDV-KIKNATIIQYQLKGLEPETAYQVDIFAENNIGSSNP 723
 724 AFSHE---LVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR 780
 341 -FSHHSAWLVVLPAEEELMETDEAGSVYAGVLSYGVVFFLFILVVAAVILCRLRSPPKKG 399
 460 ELSRTRLTLGKPLGEGCFGQVVMAEAIGIDKDRTAKPVTVAVKMLKDDATDKDLSDLVSE 519
 LEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANST 932
 506 HPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILDGY
 -----DVIGEGNFGQVLKAR---IKKD--GLRMDAAIKRMKEYASKDDHRDFAGE
 933 ASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSR---GQ
 781 MAQAF------QNVREEPAVQFNSGT-LALNRKVKNNPDPTIYPVLDWN---DIKF
 276 QPHIQWLKHVEVNGSKVG---PDGTPYV----
 1108 -YEKFTYAGIDCSAEEAA 1124
 760 PFEQYSPGGQDTPSSSSS
 A; Molecule type: mRNA
A; Residues: 1-147,150-
 A; Accession: S09953
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950 RGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSRG---QEVYVKKTMGRLPVRMMA 1006
837 QVLKARIKKDGLRMD-----AAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLL 889
 790 EEPAVQFNSGTLALN-RKVKONNPDPTIYPVLDW---NDIKFQ------DVIGEGNFG 836
 ||: | : || | | | |||||| | 491 QVVLA--EAIGLDKDKPNRVTKVAVKMLKSDATEKDLSELISEMEMMKMIGKHKNIINLL 548
 890 GACEHRGYLYLALEYAPHGNILDFIRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVA 949
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Search completed: March 14, 2006, 01:48:52 Job time : 53 secs

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Page 1

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 14, 2006, 01:40:28; Search time 253 Seconds (without alignments) 3134.442 Million cell updates/sec

US-10-633-742-8 6013 1 MDSLASLVLCGVSLLLSGTV.....TTLYEKFTYAGIDCSAEBA 1124

Title: Perfect score: Sequence:

Scoring table:

2166443 seqs, 705528306 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q02763 homo sapien		Q5tcu2 homo sapien	Q5rdb0 pongo pygma		Q8iv34 homo sapien	Q06807 bos taurus	Q02858 mus musculu	Q9qw24 rattus sp.				P35590 homo sapien	Q06805 bos taurus	Q8bgi2 m mus muscu		Q90x17 xenopus lae	Q4rj67 tetraodon n	Q9hbs4 homo sapien	Qépap2 mus musculu	Q5eh71 ovis aries			_		Q91287 pleurodeles	Q95ml3 bos taurus	Q5ttj6 anopheles g		P16092 mus musculu	Q04589 rattus norv
SUMMAKIES	TIE2 HUMAN	Q59HG2 HUMAN	QSTCU2 HUMAN	Q5RDB0_PONPY	QSRDIS_PONPY	Q8IV34 HUMAN	TIE2 BOVIN	TIEZ_MOUSE	Q9QWZ4 9MURI	Q80YS4_MOUSE	Q8IXB8_HUMAN	TIE2 BRARE	TIE1 HUMAN	TIE1_BOVIN	Q8BGI2 MOUSE	TIE1 MOUSE	Q90X17 XENLA	Q4RJ67_TETNG	Q9HBS4_HUMAN	Q6PAP2_MOUSE	QSEH71 SHEEP	TIE1 BRARE	CEK2_CHICK	090777_CHICK	Q86PM4_HYDAT	Q91287_PLEWA	Q95M13 BOVIN	Q5TTJ6_ANOGA	Q59H40_HUMAN	FGFR1 MOUSE	FGFR1_RAT
* Query Match Length DB		1157 2					•	1122 1	•	1072 2	788 2	1116 1	1138 1	1136 1	1134 2	1134 1	658 2	•			160 2					796 2			814 2		
Query Match	100.0	99.9	8.66	99.5	99.2	98.0	95.3	92.9			69.3	48.5	42.0	42.0	41.9	41.8	40.8	29.8	25.3	16.4	14.1	14.0	12.0	11.9	11.9	11.9	11.8	11.8	11.7	11.7	11.7
Score	6013	6009	0009	5981	5964.5	5890	5732.5	5584	5413	5296	4168.5	2915.5	2527	2526	2521	2515	2451	1791	1524	985	847	839	719.5	717.5	715	713.5	712.5	707.5	704	703.5	703.5
Result No.	1	2	m	4	5	9	7	œ	σ	10	11	12	13	14	15	16	11	18	19	20	21	22	23	24	25	56	27	28	29	30	31

	Q8cim9 mus musculu	042127 xenopus lae	Q7tsi8 mus musculu	Q5r8q3 pongo pygma	Q07407 drosophila	O99052 mus musculu	Q60818 mus musculu	P11362 homo sapien	Q9ps96 xenopus lae	Q8ni15 homo sapien	P22607 homo sapien	Q9psv8 xenopus lae	Q9dgk3 xenopus lae
Q9JHX9 RAT	Q8CIM9_MOUSE	042127 XENLA	Q7TSI8 MOUSE	Q5R8Q3 PONPY	FGFR1 DROME	Q99052 MOUSE	Q60818 MOUSE	FGFR1 HUMAN	Q9PS96 XENLA	Q8N115 HUMAN	FGFR3 HUMAN	Q9PSV8 XENLA	
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800	820	802	800	820	729	800	822	822	810	169	806	829	828
11.7	11.7	11.6	11.6	11.6	11.6	11.6	11.6	11.5	11.5	11.5	11.5	11.5	11.5
02.5	702.5	669	698.5	697.5	697	696.5	696.5	694.5	694	693	693	693	692.5
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## ALIGNMENTS

RESULT 1  ID _TIEZ HUMAN STANDARD, FRT; 1124 AA.  G02763.  G02763.  D1 _TIEZ HUMAN STANDARD, FRT; 1124 AA.  G02762.  D2 G02763.  D2 G02763.  D2 G02763.  D3 G02763.  D4 G02763.  D5 G02763.  D6 G02763.  D6 G02763.  D6 G02763.  D6 G02763.  D7 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763.  D8 G02763

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 MIN, 600195; C. integral to plasma membrane; TAS.

RO; GO:0000887; C. integral to plasma membrane; TAS.

RO; GO:0004872; F:protein kinase activity; TAS.

RO; GO:0004872; F:protein kinase activity; TAS.

RO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; TAS.

RO; GO:0007165; P:signal transduction; TAS.

RO; GO:0007165; P:signal transduction; TAS.

RO; GO:0007165; P:signal transduction; TAS.

RO; GO:0007165; P:signal transduction; TAS.

RO; GO:0007165; P:signal transduction; TAS.

RO; GO:0007165; P:signal transduction; TAS.

RICETPO; IPRO0426; EGF 2.

RICETPO; IPRO0426; FN TII.

RICETPO; IPRO0410; FN TII.

RICETPO; IPRO0410; FN TII.

RICETPO; IPRO0410; FN TII.

RICETPO; IPRO0410; FN TII.

RICETPO; IPRO0410; FN TII.

RICETPO; RRO0119; Prot kinase.

RICETPO; RRO010; Prot kinase.

RODOM; PRO011; FOOT kinase.

RRAT; SRO0101; PROTE kinase.

RRAT; SRO0101; PROTE Kinase.

RRAT; SRO0101; PROTE Kinase; I.

RROSITE; PSO0102; EGF 2; I.

RROSITE; PSO0102; EGF 2; I.

RROSITE; PSO0103; RROTEIN KINASE DON; I.

RROSITE; PSO0107; RROTEIN KINASE DON; I.

RROSITE; PSO0107; RROTEIN KINASE PRO; I.

RROSITE; PSO0107; RROTEIN KINASE PRO; I.

RROSITE; PSO0107; RROTEIN KINASE PRO; I.

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RROTEIN PROSITE; PSO0107; RROTEIN KINAS
 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 Angiopoletin 1 receptor.
Extracellular (Potential)
Potential.
Cytoplasmic (Potential).
 Ig-like C2-type 1.
EGF-like 1.
EGF-like 2.
EGF-like 3.
 EMBL; L06139; AAA61139.1; -; mENA.
PIR; 158388; 158388; 158388.
PDB; 1FVR; X-ray; A/B=808-1124.
Ensembl; ENSG0000120156; Homo sapiens.
HGNC; HGNC:11724; TEK.
MIM; 600195; -.
 CHAIN
TOPO DOM
TRANSMEM
TOPO DOM
DOMAIN
DOMAIN
DOMAIN
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Ig-like C2-type 2.
Fibronectin type-III 1.
Fibronectin type-III 2.
Fibronectin type-III 3.
Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
Proton acceptor (By similarity).
Phosphotyrosine (by similarity).
N-linked (GLONAC...) (Potential).
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 10-MXY-2005 (TrEMBLrel. 30, Created)
10-MXY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
TEK tyrosine kinase variant (Fragment).
Name=TEK tyrosine kinase variant;
Homo sapiens (Human)
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae,
 Gaps
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 NUCLEOTIDE SEQUENCE.
TISSUE=Brain;
TOCOKi Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama
Totoki Y., Tayoda A., Kikuno F.R.;
"None Title.";
"None Title.",
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AB208796; BAD92233.1; -; mRNA.
SWR; O59HG2; 846-1154.
 RR SMR; Q59HG2; 846-1154.

R Ensembl; ENSG00000120156; Homo sapiens.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0008201; F:heparin binding; IEA.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004713; F:protein-tyrosline kinase activity; IEA.

R GO; GO:0004713; F:protein-tyrosline kinase activity; IEA.

R GO; GO:0004672; F:receptor activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR006209; BGF_1ike.

R InterPro; IPR005209; BGF_1ike.

R InterPro; IPR005210; IEGF.
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 DB 2; Length 1157;
 1081 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEBAA 1124
 ERPSFAQILVSLNRMLBERKTYVNTTLYBKFTYAGIDCSAEBAA 1124
 1157 AA; 129275 MW; 872EFE11E6CDCF56 CRC64;
 99.9%; Score 6008; Di
99.9%; Pred. No. 0;
ative 0; Mismatches
 OS HG2 HUMAN PRELIMINARY;
 Best Local Similarity 99.9
Matches 1123; Conservative
 Homo.
NCBI_TaxID=9606;
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 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1020
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 540
 300
 360
 420
 421 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK 480
 600
 909
 9
 720
 720
 780
 780
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 61 PEALANQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKWRQ 120
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 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK 480
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 LINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
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 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 LLINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 Gaps
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 Length 1124;
 0; Indels
1124 AA; 125811 MW; 65BC05D18FA4CCBC CRC64;
 DB 1;
 Query Match
100.0%; Score 6013;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1124; Conservative 0; Mismatches
 61
 241
 661
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 721
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SEQUENCE
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120
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 121 QASFLPATLTWTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH 180
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 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
 61 FEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRO
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCTASGWRPHEPITIGRD
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 Gaps
 REMEL, ALSSASIS, CALIGOES.1; JOINED; Genomic_DNA.

REMEL, ALSSASIS, CALIGOES.1; JOINED; Genomic_DNA.

REMEL, ALSSASIS, CALIGOES.1; JOINED; Genomic_DNA.

RESEMBL; ENSGOOO0120156; Homo sapiens.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein exine kinase activity; IEA.

GO; GO:0004713; F:protein amino acid phosphorylation; IEA.

InterPro; IRRO0342; EGF_like.

InterPro; IRRO0342; EGF_like.

InterPro; IRRO0342; FPC kinase.

InterPro; IRRO0310; IGF.

InterPro; IRRO0310; IGF.

InterPro; IRRO0345; TYL_pkinase.

InterPro; IRRO0345; TYL_pkinase.

InterPro; IRRO0345; TYL_pkinase.

InterPro; IRRO0345; TYL_pkinase.

InterPro; IRRO0345; TYL_pkinase.

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INTERPRO; IRRO0345; TYL_pkinase.

INTERPRO; IRRO0345; TYLC: 1.

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INTERPRO; IRRO0345; TYLC: 1.

INTERPRO; IRRO0345; TYLC: 1.

INTERPRO; IRRO0345; TYLC: 1.

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01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
TEX tyrosine kinase, endothelial (Venous malformations, multiple
cutaneous and mucosal).
 ö
 1157
 Indels
 Corby N.;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
 1124 AA; 125830 MW; E739DEC3E4FEB124 CRC64;
1114 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA
 DB 2;
 EMBL; AL133411; CAI16055.1; -; Genomic DNA.
EMBL; AL355432; CAI16055.1; JOINED; Genomic DNA.
EMBL; AL355433; CAI16055.1; JOINED; Genomic DNA.
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 99.8%; Score 6000; Di
99.8%; Pred. No. 0;
iive 0; Mismatches
 Query Match
Best Local Similarity 99.8°
Matches 1122; Conservative
 QSTCU2 HUMAN PRELIMINARY;
 Homo sapiens (Human)
 NUCLEOTIDE SEQUENCE.
 NCBI_TaxID=9606;
 SEQUENCE
 Kinase
 RESULT
QSTCU2_
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 994 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1053
 1HRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1020
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 VNSGKFNPICKASGWPLPINEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG 420
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 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE 333
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE 360
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVULPDHIE 393
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 753
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 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL 933
 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF 960
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 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKK
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 394
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 661
 1021
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 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1020
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 LLYKPVNHYEAMQHIQVTNEIVTLAYLEPRTEYELCVQLVRRGEGGEGHPGPVRRPTTAS
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 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPPTIXPVLDMNDIKFQDVIGEGNFGQVLK
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 ICPPGFMGRTCEKACELHTFGRTCKBRCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 541 IGLPPPRGLNLLPKSQTTLNLTHQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
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 ARIKKOGLRMDAAIKRMKEYASKODHRDFAGELEVICKIGHHPNIINLLGACEHRGYLYL
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 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
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 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE 300
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 NUCLEOTIDE SEQUENCE.

TISSUE=Kidney;

THe German cDNA Consortium;

Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,

Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CRESSO04; CAH90247.1; -; mRNA.
 Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
 1 MDSLASLVLCGVSLLPSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 ICPPGFMGRICEKACELHIFGRICKERCSGQEGCKSYVPCLPDPYGCSCATGWKGLQCNE
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
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 RMBL; CRESSOOQ; CAH90247.1; -; MANA.

RMR; OSRDBO; 813-112.1

CO; GO:0005524; F:ATP binding; IEA.

CO; GO:0004674; F:ATP binding; IEA.

CO; GO:0004674; F:Procein serine-(threonine kinase activity; IEA.

CO; GO:0004674; F:procein serine-(threonine kinase activity; IEA.

CO; GO:0004619; F:procein amino acid phosphorylation; IEA.

RO; GO:0005198; P:procein amino acid phosphorylation; IEA.

RR GO; GO:0005409; P:procein amino acid phosphorylation; IEA.

RR InterPro; IPR000742; EGF_1ike.

RR InterPro; IPR0003961; RN III.

RITERPO; IPR0003961; ROF—IIKe.

RR InterPro; IPR00110; Ig-like.

RR InterPro; IPR001245; Tyr_pkinase.

RR InterPro; IPR001245; Tyr_pkinase.

RR InterPro; IPR001245; Tyr_pkinase.

RR ProDom; PR00041; FO; Tyr_pkinase.

RR ProDom; PR00041; EGF_3:

RR SMART; SM00060; FN3; 3.

RR SMART; SM00060; FN3; 3.

RR SMART; SM00060; FN3; 3.

RR SMART; SM00124; Tyr_C; 1.

RR PROSITE; PS01025; EGF_1; 3.

RR PROSITE; PS01025; EGF_1; 3.

RR PROSITE; PS01025; EGF_1; 3.

RR PROSITE; PS01017; PROTEIN KINASE ATP; 1.

RR PROSITE; PS01017; PROTEIN KINASE_DOM; 1.

RR PROSITE; PS01017; PROTEIN KINASE_TYR; 1.
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 DB 2; Length 1124;
 Indels
 125926 MW; A771C45B94F09AA2 CRC64;
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp469L125.
Name=DKFZp469L125;
 Query Match
99.5%; Score 5981; D
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1117; Conservative 2; Mismatches
 Hypothetical protein.
SEQUENCE 1124 AA;
 NCBI_TaxID=9600;
 SEQUENCE
 181
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(TrEMBLrel. 29, Created) (TrEMBLrel. 29, Last sequence update)

DBO PONPY
OSRDBO PONPY PRELIMINARY;
OSRDBO;
01-PEB-2005 (TREMBLEEL 29,
01-PEB-2005 (TREMBLEEL 29,

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 121 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 QASFLPATITIMITYDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
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 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 181 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 Gaps
 Wiemann
 The German cDNA Consortium;

The German cDNA Consortium;

Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaipp A., Bewestler B., Obermaier B., Deutschenbaur S., Schaipp A., Bewestler B., Obermaier B., Deutschenbaur S., Schaipp A., Enbaitted (NOV-2004) to the ENBL/GenBank/DDBJ databases.

BRB1, CRB57924; CAH90172.1; -; mRNA.

BRM1, ORNDIS; 812-1120.

GO; GO:0006574; F:Protein erine/threonine kinase activity; IEA.

GO; GO:0006734; F:Protein erine/threonine cativity; IEA.

GO; GO:0006734; F:Protein erine/threonine activity; IEA.

GO; GO:0006738; F:Protein erine/threonine activity; IEA.

GO; GO:0006738; F:Protein erine/threonine activity; IEA.

GO; GO:0006738; F:Protein erine/threonine activity; IEA.

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GO; GO:0006738; F:Protein erine/threonine activity; IEA.

GO; GO:0006738; F:Protein erine/threonine activity; IEA.

InterPro; IPRO0030; EGF_1:

InterPro; IPRO0030; F:Protein erine

InterPro; IPRO0030; F:Protein erine

InterPro; IPRO0041; F:Protein erine

InterPro; IPRO0041; F:Protein erine

InterPro; IPRO0041; F:Protein erine

InterPro; IPRO0041; F:Protein erine

InterPro; IPRO0041; F:Protein erine

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INTERPRO; IPRO0041; F:Protein erine

INTERPRO; IPRO0041; F:Protein erine

INTERPRO; IPRO0041
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 Length
 4; Indels
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 Query Match
99.2%; Score 5964.5;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1117; Conservative 2; Mismatches
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UNKNOWN_3
 PRINTS; PRO0109; TYRKINASE.
PRODOM; PD000001; Prot_kinase; 1.
SMART; SM00181; EGF; 2.
SMART; SM00060; FN3; 3.
SMART; SM00219; TYTKC; 1.
 PROSITE; PS00022; EGF 1; UNN
PROSITE; PS01186; EGF 2; 3.
PROSITE; PS50026; EGF 3; 1.
PROSITE; PS50853; FN3; 3.
 Best Local Similarity 99.7 Matches 1098; Conservative
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 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGWTCLTVLLAFLIILQLKRANVQRR
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV
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 LIANNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
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 781 MAQAFQN-REEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK
 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD
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 AI EYAPHGNILLDFLRKSRVLETDPAFAI ANSTASTLSSQQLLHFAADVARGMDYLSQKQF
 1080 ERPSFAQILVSLARMLEERKTYVVTTLYEKFTYAGIDCSAEEAA 1123
 ERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 Last sequence update)
Last annotation update)
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 OBIV34 HUMAN PRELIMINARY;
OBIV34 HUMAN PRELIMINARY;
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O1-MAR-2004 (TrEMBLrel. 26, Le
TEK PACCEIN.
Name=TEK;
Homo sapiens (Human).
 NCBI_TaxID=9606;
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 324 DRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIEVNSGKFNPICKASGWPLPTNEEM 383
 83
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W., Villadon D.K., Nuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schotiguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnetch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., "Generch A., Schein J.E., Jones S.J.M., Marra M.A.;
 1 MDLILINSLPLVSDAETSLTCIASGWRPHEFITIGRDFEALMNQHQDFLEVTQDVTREWA
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 24 MDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRDFEALMNQHQDPLEVTQDVTREWA
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 CKERCSGOEGCKSYVPCLPDPYGCSCATGWKGLQCNEACHPGPYGPDCKLRCSCNNGEMC
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 TISSUE=Parceas;

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INTH MGC Project;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC035514; AA435514.1; -; mRNA.

HSSP; Q02763; 1FVR.

R SMR; Q01704; 790-1098.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein ryrosine kinase activity; IEA.

GO; GO:0004713; F:protein amino acid phosphorylation; IEA.

InterPro; IPR005209; BGF_like.

R InterPro; IPR005209; BGF_like.

R InterPro; IPR00510; IEGF.

R InterPro; IPR007110; Ig-like.

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R InterPro; IPR007110; Ig-like.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001246; Tyr_pkinase.

R Pfenn; PF00041; fin3; 3.
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ive 0; Mismatches 3; Indels
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PROSITE; PSOB109; PROTEIN KINASE TYR; 1.
SEQUENCE 1101 AA; 123599 MW; C9DF2721F767B0D0 CRC64;
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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 GLSRGQEVYVKKTMGRLPVRMMAIESLNYSVYTTNSDVWSYGVLLMEIVSLGGTPYCGMT 1020
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NUCLEOTIDE SEQUENCE
 NCBI_TaxID=9913;
 301
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMML outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
MEDLINE=9402374; PubMed=8415706;
Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
Tie-1 and tie-2 define another class of putative receptor tyrosine kinase genes expressed in early embryonic vascular system.";
Proc. Natl. Acad. Sci. U.S.A. 90:9355-9358(1993).
I- FUNCTION: This protein is a protein tyrosine-kinase transmembrane receptor for angiopoietin 1. It may constitute the earliest mammalian endothelial cell lineage marker. Probably regulates endothelial cell proliferation, differentiation and guides the formation.

Example 1. Example 1. Example 1. Example 1. Example 2. Example 2. Example 2. Example 3
 Probom, PD00001, Proc Kinase; 1.

R SWART; SM00180; EGF Lam; 1.

R SWART; SM00180; EGF Lam; 1.

R SWART; SM00180; EGF Lam; 1.

R SWART; SM00180; EGF Lam; 1.

R PROSITE; PS01022; EGF 1; 3.

R PROSITE; PS010186; EGF 2; 2.

R PROSITE; PS01010; PROTEIN KINASE ATP; 1.

R PROSITE; PS01010; PROTEIN KINASE DOW; 1.

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R PROSITE; PS01019; PROTEIN KINASE DOW; 1.

R PROSITE; PS01019; PROTEIN KINASE DOW; 1.

R PROSITE; PS01019; P
 tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: Specifically expressed in developing vascular
 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 -1- SIMILARITY: Contains 3 EGF-like domains.
-1- SIMILARITY: Contains 3 fibronectin type-III domains.
-1- SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like) domains.
 endothelial cells.
 Angiopoietin 1 receptor.
Extracellular (Potential)
 Ig-like C2-type 2.
Fibronectin type-III 1.
Fibronectin type-III 2.
Fibronectin type-III 3.
 Potential.
Cytoplasmic (Potential)
 Ig-like C2-type 1.
EGF-like 1.
EGF-like 2.
EGF-like 3.
 EMBL; X71424; CAA50555.1; -; mRNA. PIR; S57846; S57846. HSSP; Q02763; IPVR. SMR; Q06807; 814-1122. InterPro; IPR000742; EGF 2. InterPro; IPR005209; EGF like. InterPro; IPR001361; FN III. InterPro; IPR00110; IG-like. InterPro; IPR00110; IG-like. InterPro; IPR00110; IG-like. InterPro; IPR00119; Prot kinase. InterPro; IPR001245; Tyr pkinase. InterPro; IPR001245; Tyr pkinase. Pfom1; Pr00041; fn3; 3.
 PRINTS; PR00109; TYRKINASE
 1125
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QASFLPATLTMTVDKGDNVNISFKKVLIKBEDAVIYKNGSPIHSVPRHEVPDILEVHLPH 180
 ICPPGFMGRICEKACELHTFGRICKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE 300
 1 MDSLAGLVLCGVSLLLYGVVEGAMDLILINSLPLVSDAETSLTCIASGWHPHEPITIGRD 60
PROSITE; PS00022; EGF 1; 3.

DR PROSITE; PS00026; EGF 2; 3.

DR PROSITE; PS50853; FN3; 3.

DR PROSITE; PS50853; FN3; 3.

DR PROSITE; PS50815; FN3; 3.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE DOM; 1.

DR ATP-binding; EGF-like domain; Glycoprotein; Immunoglobulin domain; KW Kinase; Multigene family; Nucleotide-binding; Phosphorylation; KW Receptor; Repeat; Signal; Transferase; Transmembrane; Transferase; Transmembrane; Transferase; Transmembrane; Transmembra
 AQPODAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
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A -> G (in Ref. 1 and 4).
MLLIAILGSAGMTCITV -> DATHSHPWWNDFASPC
 ATP (By similarity).
Phosphotyrosine (by autocatalysis)
 EGF-like 2.
EGF-like 3.
EGF-like 3.
Ig-like C2-type 2.
Ig-like C2-type 2.
Fibronectin type-III 1.
Fibronectin type-III 2.
Fibronectin type-III 3.
Protein kinase.
ATP (By similarity).
Proton acceptor (By similarity).
 92.9%; Score 5584; DB 1; Length 1122; 92.7%; Pred. No. 8.4e-312; Live 37; Mismatches 41; Indels 4
 (in Ref. 3).
N -> NV (in Ref. 3 and 6).
R -> G (in Ref. 3).
ALANGTA -> CHRQOYS (in Ref. 3).
S -> P (in Ref. 3).
 786 786 N -> NV (in Ref. 3 and 6).
913 913 R -> G (in Ref. 3).
925 931 AIANSTA -> CHRQQYS (in Ref.
117 1117 -> P (in Ref. 3).
1122 AA; 125701 MW; F879623D103FFE96 CRC64;
 Angiopoietin 1 receptor.
Extracellular (Potential)
Potential.
 Cytoplasmic (Potential).
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 [g-like C2-type 1.
 EGF-like 1.
 similarity)
 N-linked
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 Best Local Similarity 92.78
Matches 1043; Conservative
 535
535
632
730
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836
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 ACT SITE
BINDING
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 Dumont D.J., Yamaguchi T.P., Conlon R.A., Rossant J., Breitman M.L.,
"Tek, a novel tyrosine kinase gene located on mouse chromosome 4, is
expressed in endothelial cells and their presumptive precursors.";
Oncogene 7:1471-1480(1992).
-!- FUNCTION: This protein is a protein tyrosine-kinase transmembrane
receptor for angiopoietin 1. It may constitute the earliest
mammalian endothelial cell lineage marker. Probably regulates
endothelial cell proliferation, differentiation and guides the
proper patterning of endothelial cells during blood vessel
formation.
 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Specifically expressed in developing vascular endothelial cells. Abundantly expressed in lung and heart, andorately in brain, liver and kidney, and weakly in thymus, spleen and testis.

DEVELOPMENTAL STAGE: Expression detectable in day 8.5 embryos.
 "Molecular cloning and characterization of mouse TIE and TEK receptor tyrostne kinase genes and their expression in hematopoietic stem cells.";
Biochem. Biophys. Res. Commun. 195:301-309(1993).
 SIMILĀRITY: Contains 3 EGF-like domains.
SIMILĀRITY: Contains 3 fibronectin type-III domains.
SIMILĀRITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
domains.
 Iwama A., Hamaguchi I., Hashiyama M., Murayama Y., Yasunaga K.,
Suda T.;
 EMBL; X71426; CAA50557.1; -; mENA.

EMBL; X67553; CAA4857.1; -; mENA.

EMBL; D13738; BAA02883.1; -; mENA.

EMBL; D13738; BAA02883.1; -; mENA.

EMBL; D03763; 1FVR.

SMR; Q02763; 1FVR.

SMR; Q02864; 11-1119.

Ensembl; ENSMUSG0000006386; Mus musculus.

MGT; MGT: 98664; Tek.

GG; GG:0005615; C:extracellular space; TAS.

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GG; GO:0007160; P:cell-marrix adhesion; IMP.

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GG; GO:0007160; P:cell-marrix adhesion; IMP.

R GG; GO:0007160; P:cell-marrix adhesion; IMP.

GG; GO:0007160; P:cell-marrix adhesion; IMP.

R InterPro; IPR0007042; EGF 2.

InterPro; IPR000719; P:cell-minin EGF.

InterPro; IPR000719; Prot Kinase.

InterPro; IPR00149; Prot Kinase.

InterPro; IPR00141; FN; Tyrinase AS.

Pfem: PF00041; fn3; 3.
 NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY
 NUCLEOTIDE SEQUENCE OF 822-1122.
STRAIN=CD-1; TISSUE=Embryonic heart;
MEDLINE≈92334855; PubMed=1630810;
 PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot kinase; 1.
SWRAT; SW00180; BGF Lam; 1.
SWART; SW00060; FN3; 3.
SWART; SW00219; TYFKC; 1.
 ISSUE=Hematopoietic stem cells;
 Pfam; PF00041; fn3; 3.
 PubMed≈8395828
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 1 TSLTCIASGWHPHEPITIGRDFEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGA
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 40 TSLTCIASGWRPHEPITIGRDFEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGA
 Gaps
 MEDLINE-92775658, PubMed=7684830;
Maisonpierre P.C., Goldfarb M., Yancopoulos G.D., Gao G.;
Maisonpierre P.C., Goldfarb M., Yancopoulos G.D., Gao G.;
Tolstinct rat genes with related profiles of expression define a TII receptor tyrosine kinase family.";
Oncogene 8:1631-1637(1993).

In Mark, Ogowa4; 772-1080.

R SMR, Ogowa4; 772-1080.

GO; GO:000524; F:ATP binding; IEA.

GO; GO:000524; F:ATP binding; IEA.

GO; GO:0005198; F:structin-tyrosine kinase activity; IEA.

GO; GO:000548; F:structural molecule activity; IEA.

GO; GO:000548; F:structural molecule activity; IEA.

R InterPro; IPR000509; EGF_like.

InterPro; IPR000509; EGF_like.

InterPro; IPR000719; FV III.

InterPro; IPR000719; Prot kinase.

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InterPro; IPR000719; Prot kinase.

InterPro; IPR000266; Tyr_pkinase.

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InterPro; IPR000266; Tyr_pkinase.

InterPro; IPR00041; fm3, 3.yr_pkinase.

InterPro; IPR00041; fm3, 3.yr_pkinase.

InterPro; IPR00041; fm3, 3.yr_pkinase.

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InterPro; IPR00041; fm3, 3.yr_pkinase.

InterPro; IPR00041; fm3, 3.yr_pkinase.

InterPro; IPR00041; fm3, 3.yr_pkinase.
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 RELINTS; PRO0101; TYRKINASE.

RELINTS; PRO0101; Prot kinase; 1.

RELINTS; SMO0109; EPCt kinase; 1.

RELINT; SMO01019; EFCT Lam; 1.

RELINT; SMO0119; TYRKC; 1.

RELINT; SMO0129; TYRKC; 1.

RECOSTIE; PSS0012; EGF 2; 1.

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RECOSTIE; PSS0119; PROTEIN KINASE ATP; UNKNOWN 1.

RECOSTIE; PSS0110; PROTEIN KINASE TYR; 1.

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RECOSTIE; PSC0110; PROTEIN KINASE TYR; 1.
 90.0%; Score 5413; DB 2; 93.0%; Pred. No. 5.3e-302; ive 30; Mismatches 38;
 Best Local Similarity 93.08
Matches 1012; Conservative
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 KARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLY
 KARIKKOGLRMDAAIKRMKEYASKODHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLY
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 LAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQ
 FIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNS
 FIHRDLAARNILVGENYIAKIADFGLSRGQEVYVKKTWGRLPVRWMAIESLNYSVYTTNS
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 LEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGI 1116
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 CKLGHHPNI INLLGACEHRGYLYLAI EYAPHGNLLDFLRKSRVLETDPAFAIANSTASTL
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 TISSUE=EmbryO;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge U.G.,
Straubberg R.L., Feingeold E.A., Grouse L.H., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RRSVQ-KSDQQNIKVPGNLTSVLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTL--SD
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 1016 LEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGI
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Last sequence update)
Last annotation update)
 PRT; 1072 AA.
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 YS4 MOUSE
QBOYS4 MOUSE PRELIMINARY;
QBOYS4;
QL-UN-2003 (TEMBLEE]: 24, C:
Q1-UN-2003 (TEMBLEE]: 24, L:
Q1-MAR-2004 (TEMBLEE]: 26, L:
 DCSAEEAA 1124
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 Mus musculus (Mouse)
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 Tek protein.
Name=Tek;
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones G. More than 15,000 full-length human
 1 MDSLAGLVLCGVSLLLYGVVEGAMDLILINSLPLVSDAETSLTCIASGWHPHEPITIGRD
 61 FEALMNOHODPLEVTODVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRO
 QASFLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH
 241 ICPPGFMGRICEKACELHIFGRICKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 181 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 ------ceaokwepocsrpcitcknievchedicec
 Gaps
 54;
 Length 1072;
 EMBL; BCO50824; AAH50824.1; -; mRNA.

Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

R H5SP; QO2763; IFVR.

R H5SP; QO2763; IFVR.

R GOSPS; QO2000006186; Mus musculus.

R MG1; MG1:98664; Tek.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:0016021; C:attregral to membrane; TAS.

GO; GO:00160216; P:regulation of cell migration; IMP.

R InterPro; IPR000710; Ig-like.

R InterPro; IPR000710; Ig-like.

R InterPro; IPR000710; Ig-like.

R InterPro; IPR000710; Ig-like.

R InterPro; IPR000710; Ig-like.

R InterPro; IPR000710; Ig-like.

R InterPro; IPR000710; Ig-like.

R InterPro; IPR000710; Ig-like.

R PR00171; FR001
 Query Match 88.1%; Score 5296; DB 2; Length 1
Best Local Similarity 88.3%; Pred. No. 2.7e-295;
Matches 993; Conservative 37; Mismatches 41; Indels
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Teuteumi
 Jin C., Sueishi X., Journal I., Jingling I., Janil M., 18
Li Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBLA ABOSESS BAC45250.1; -; mRNA.

EMBLA ABOSESS BAC45250.1; -; mRNA.

ENSEMBL; RSCG0000120156; Homo sapiens.

GO; GO:0004872; F:receptor activity; IEA.

RO; GO:0004872; F:receptor activity; IEA.

RICEPTO; IPR000742; EGF_like.

RICEPTO; IPR0005209; EGF_like.

RICEPTO; IPR000510; IEGF.

INTERPO; IPR000110; Ig-like.

RICEPTO; IPR00110; Ig-like.

REPTOSTITE; PS00024; EGF_1; UNKNOWN_2.

REPROSTITE; PS00026; EGF_2; 2.

REPROSTITE; PS00026; EGF_2; 1.

REPROSTITE; PS00026; EGF_2; 1.

REPTOSTITE; PS00026; EGF_2; 1.

REPTOSTITE; PS00026; EGF_2; 1.

REPTOSTITE; PS00026; EGF_2; 1.

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REPTOSTITE; PS00026; EGF_2; 1.

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REPTOSTITE; PS00026; EGF_2; 1.

REPTOSTITE; PS00026; EGF_3; 1.

REPTOSTITE; PS00026; EGF_3; 1.

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REPTOSTITE; PS00026; EGF_3; 1.

REPTOSTITE; PS00026; EGF_3; 1.

REPTOSTITE; PS00026; EGF_3; 1.

REPTOSTITE; PS00026; EGF_3; 1.
Sata S., Nakagawa K., Yonemitsu Y., Onimaru M., Tanii M., Jin C., Sueishi K.; Sueishi K.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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 DVWSYGVILWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKP 1027
 FIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNS 1019
 DVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKP 1079
 480
 369
 540
 599
 429
 487
 629
 607
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 196
 547
 667
 727
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 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
 FIHRDLAARNILVGENYIAKIADFGLSRGQEVYVKKTMGRLPVRMAIESLNYSVYTTNS
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 ACPSGYYGPDCKLRCHCTNEICDRFQGCLCSQGWQGLQCEKEGRPRMTPQIEDLPDHIE
 LLYKPVNHYBAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 VLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISW
 TILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIG
 SSNPAFSHELVTLPESQAPADIGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQR
 RMAQAFQNVREEPAVQFNSGTLALNRKAKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVL
 UNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
 IGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQ-KSDQQNIKVPGNLTS
 RMAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPT1YPVLDWND1KFQDV1GEGNFGQVL
 KARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLY
 KARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLY
 1028 YERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEBAA 1072
 1080 YERPSFAQILVSIARMLEERKTYVATTLYEKFTYAGIDCSAEBA 1124
 OBIXBB HUMAN PRELIMINARY; PRT; 788 AA.
QBIXBB;
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Receptor protein tyrosine kinase (Fragment).
Name=Tie-2;
 Homo sapiens (Human).
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NUCLEOTIDE SEQUENCE
 NCBI_TaxID=9606;
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 RESULT 11
081XBB HUMAN
1D Q81XBB HUMAN
1D Q81XBB HUMAN-21
DT 01-MAR-21
DT 01-MAR-21
DB Receptor
GN Name=Tie
OC Blastyou-
CC Mammalia
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OC NCBI Tax
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360 617 240 240 120 120 180 180 299 317 420 377 480 437 540 497 900 557 9 9 9 61 FEALANQHQDPLEVTQDVTREWAKKVWKREKASKINGAYFCEGRVRGEAIRIRITMKARQ 121 QASFLPATLTWTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH 181 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC 241 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE 241 ICPPGFMGRICEKACELHTFGRICKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCN-301 ACHPGFYGPDCKLRCSCNNGBMCDRFQGCLCSPGWQGLQCBRBGIPRMTPKIVDLPDHIB 361 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG 318 VNSGKRNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD 61 FEALMNOHODPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKWRQ QASFLPATLIMIVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPH AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC LLYKPVNHYBAWQHIQVTNEI VTLNYLEPRTEYBLCVQLVRRGEGGEGHPGPVRRFTTAS Gaps 43; Query Match 69.3%; Score 4168.5; DB 2; Length 788; Best Local Similarity 94.8%; Pred. No. 9.7e-231; Matches 788; Conservative 0; Mismatches 0; Indels 43;

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62 QEPPRPQGSVLALGQEF----PHTEPRPHPAAATVTWSSR-----SHAFGAFYCQI 108
 105 RVRGEAIRIRTMKWRQQASFLPATLTWTVDKGDNVNISFKKVLIKEEDAVIYKWGSFIHS 164
SMART; SM00181; EGF; 2.

SMART; SM0000; IG; 13.

SMART; SM00109; IG; 1.

SMART; SM00129; TYRC; 1.

SMART; SM00129; TYRC; 1.

RAPOSITE; PS01021; EGF 1; 2.

RAPOSITE; PS01016; EGF 2; 2.

RAPOSITE; PS01017; PROFEIN KINASE ATP; 1.

RAPOSITE; PS01017; PROFEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

TYPOSING-PROFEIN KINASE; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.

TYPOSING-PROFEIN KINASE; 1.

RAPOSITE; PS01019; PROTEIN KINASE DOM; 1.
 165 VPRHEVPDILEVHLPHAQPQD-AGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHL
 CPRCANGGVCDDTTGECVCPPGFRGHTCDIVCGEGRFGAGCKERC--VDGVCRALVFCLR
 DPYGCSCATGWKGLQCNEACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCER
 4 LDSCTALLILG--CMMSGSAVRISDVTLVNPDPVVSPLTAPSLLCVSSDWSSGGSVLALG
 CTACMINGVCHEDIGECICPPGFMGRICEKACELHIFGRICKERCSGQEG-CKSYVFCLP
 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSD-AETSLTCIASGW-----
 ----RPH-EPITIGRDFEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEG
 Tyrosine-protein kinase receptor Tie-2
Extracellular (Potential).
 Proton acceptor (By similarity).
ATP (By similarity).
Phosphotyrosine (by autocatalysis)
 tch 48.5%; Score 2915.5; DB 1; Length 1116; al Similarity 51.6%; Pred. No. 1.3e-158; 596; Conservative 173; Mismatches 311; Indels 75;
 122361 MW; AA414E8C745A8937 CRC64;
 Cytoplasmic (Potential). Ig-like C2-type 1.
 EGF-like 1.
EGF-like 2.
EGF-like 3.
Ig-like C2-type 2.
Ig-like C2-type 2.
Fibronectin type-III 1.
Fibronectin type-III 3.
 N-linked (GlCNAC...)
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 Protein kinase.
ATP (By similarity).
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 Potential
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 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR 737
 618 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIPAENNIGS
 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR
 ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
14-SEP-2005 (Rel. 48, Last annotation update)
15-SEP-2005 (Rel. 48, Last annotation (Rel. 2.7.1.112).
15-SEP-2005 (Rel. 48, Last annotation (Rel. 2.7.1.112).
15-SEP-2005 (Rel. 48, Last annotation (Rel. 2.7.1.112).
16-SEP-2005 (Rel. 48, Last annotation (Rel. 2.7.1.112).
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 tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR SPECIFICITY: Expressed in most populations of endothelial cells in 24 hours embryos. Not present in intersegmental vessels SIMILARITY: Belongs to the Tyr protein kinase family. Tie
 Dev. Dyn. 212:133-140(1998).

-I- FUNCTION: Probably regulates endothelial cell proliferation, differentiation and guides the proper patterning of endothelial cells during blood vessel formation (By similarity).

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 MEDLINE-99264593; PubMed-9603430; DOI-10.1002/(SICI)1097-0177(199805)212:14:133::AID-AJA12>3.3.CO;2-3; DOI-10.1002/(SICI)1097-0177(199805)212:14:133::AID-AJA12>3.3.CO;2-3; Lyong M.S., Bell B., Stainler D., Peters K.G.; "Isolation of the zebrafish homologues for the tie-1 and tie-2 endothellum-specific receptor tyrosine kinases.";
 MAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIG 788
 SIMILARITY: Contains 3 EGF-like domains.
SIMILARITY: Contains 3 fibronectin type-III domains.
SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
 MAQAFQNIVREEPAVQFINSGTLALINRKVKNNNPDPT1YPVLDWND1KFQDV1G
 NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY TISSUE=Embryo;
 EMBL, AF053632; AAC09331.1; -; mRNA.
HSSP, Q02763; 1FVR.
SMR; Q073791; 907-111; -; mRNA.
ZFNY, ZDB-GENE-990415-56; tie2.
INTERPTO; 1PR000742; EGF_2.
INTERPTO; 1PR005209; EGF_like.
INTERPTO; 1PR005209; EGF_like.
INTERPTO; 1PR003509; IGF.
INTERPTO; 1PR007110; IGF.
INTERPTO; 1PR007110; IG-like.
INTERPTO; 1PR007110; IG-like.
INTERPTO; 1PR007110; IG-like.
INTERPTO; 1PR007110; IG-like.
INTERPTO; 1PR001245; TYT_Pkinase.
Pf-m. PF00041; FN3.
 PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
 STANDARD;
 Pfam; PF00041; fn3; 3
 subfamily
 domains.
 TIE2 BRARE
ID TIE2 BRARE
AC 073791;
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(Potential).
(Potential).
(Potential).
(Potential).
(Potential).

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NUCLEOTIDE SEQUENCE.
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 TISSUE=Lung;
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 EKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLY 1108
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 344 AD---SSPVISHLRD-VEINTGVELSVNCSASGRPAPLHGDITLITANRTTIAAVDTHTL 399
 634
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 754
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
 EKLPLGPRLEKPLNCDDEVYELMQQCWREKPFBRPSFSQILLSLGRMLEBRKTYVNTTLY
 EGIPRATPKI VDLPDHIEVNSG-KFNPICKASGWPLPTNEEATLVKPDGTVLHPKDFNHT
 SVQKSDQQNIKVPGNLTSVLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQ
 : :: | | :: | | :: | | : | AGAPGTLRTFQLPSNSSAMFLSDLKPRHKYQCTVR-SSCGVGQNHPSASAWTLSDQLPPP
 PENIKISNITHSSAVISWTILDGYSISSITIRY-KVQGKNEDQHVDVKIKNATI-IQYQL
 QEVYVKKTMGRL PVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELY
 DHPSVAIFTIHRILPPDSGVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFA
 VINISSEPYFGDGPIKSKKLLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVR
 RGEGGEGHPGPVRRFTTASIGLPPPRGLNLLPKSQTTLNLTWQPIPPSSEDDFYVEVERR
 KGLEPETAYQVDI FAENNI GSSNPAFSHELVTLPESQAPADLGG-GKMLLIAILGSAGMT
 CITVLLAPLILLQLKRANVQRRMAQAFQNVREEPAVQFNSGTLALNRKVKNNPDP-----
 CCTVLLAFCIVLQLKRNTLQRRIHSI - - - LREEPAVHFSSA - - - - - - - PPPHRRSA
 ----TIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRD
 PAGELEVLCKLGHHPNI INLLGACEHRGYLYLAI EYAPHGNLLDFLRKSRVLETDPAFAI
 ANSTASTLSSQQLLHFAADVARGMDYLSQKQF1HRDLAARN1LVGENYVAK1ADFGLSRG
 TIEL HUMAN
AC P3550;
DT 01-UNN-1994 (Rel. 29, Created)
DT 01-UNN-1994 (Rel. 29, Last sequence update)
DT 01-UNN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DT 13-SEP-2005 (Rel. 29)
DE Tyrosine-protein kinase receptor Tie-1 precursor (EC 2.7.1.112).
GN Name=TIE1; Synonyms=TIE;
OS Homo sapiens (Human).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominid OC Homo.
OX NCBI_TaxID=9606;
RN [1]
 EKFTYAGIDCSAEEA 1123
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 TAS
 verified cleavage sites.";
protein Sci. 13:2819-2824(2004).
-!- FUNCTION: Probable protein tyrosine-kinase transmembrane receptor.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
 tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: Specifically expressed in developing vascular
 Ξ.
 GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .
GO; GO:0007498; P:mesoderm development; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR
MEDLINE=92195316; PubMed=1312667;
Partanen J., Armstrong B., Maekelae T.P., Korhonen J., Sandberg Renkonen R., Knuutla S., Huebner K., Alitalo K.;
"A novel endothelial cell surface receptor tyrosine kinase with extracellular epidermal growth factor homology domains.";
Mol. Cell. Biol. 12:1698-1707(1992).
 -!- SIMILARITY: Contains 3 EGF-like domains.
-!- SIMILARITY: Contains 3 fibronectin type-III domains.
-!- SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 PROTEIN SEQUENCE OF 22-36.
PubMed=15340161, DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.:
"Signal peptide prediction based on analysis of experimentally
 endothelial cells.
 Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 SMR; P35590; 828-1136.
Ensembl; ENSG0000066056; Homo sapiens.
 NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA)
 EMBL; X60957; CAA43290.1; -; mRNA.
EMBL; BC038239; AAH38239.1; -; mRNA.
 HGNC; HGNC:11809; TIE1.
 SEQUENCE REVISION.
 subfamily
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805 820 865 880

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1001 SRGEEVYVKKTMGRLPVRMMAIESLNYSVYTTKSDVMSFGVLLWEIVSLGGTPYCGMTCA 1060
 ELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNT 1105
 KISNITHSSAVISW----TILDGYSISSITIRYKVQGKNEDQ---HVDVKIKNATIIQYQL 699
 GWWCSWNTWAGMVEKPFNISWKVLPKPLNAPNVIDTGHNFAVIN--ISSEPYFGDGPIK 477
 241 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 TTASIGLPPPRGLNLLP-----KSQTTLNLTWQ-PIFPSS--EDDFYVEVERRSVQKS
 806 KVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDD
 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 361 VNSGKFNPI-CKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDS
 362 FNLETMPRINCAAAGNPFPVRGSIELRKPDGTVLLSTKAIVEPEKTTAEFEVPRLVLADS
 700 KGLEPETAYQVDIFA------ENNIGSSNPAFSHELVTLPESQAPADLGGGXM
 LLIAILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQN-VREEPAVQFNSGTLALNR
 SKKLLYKPVNHYEAWQHIQV-TNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRF
 587 DQQNIKVPGNLTSVLLNNLHPREQYVVRARV-NTKAQGEWSEDLTAWTLSDILPPQPENI
 SRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCA
 PAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGL
 (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 48, Last annotation update)
 PRT; 1136 AA
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SLFENFTYAGIDATAEEA 1138
 1106 TLYEKFTYAGIDCSAEEA 1123
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DT 01-FEB-1995 (DT 01-FEB-1995 (DT 13-SEP-2005) (DT 13-SEP-2005) (DT 01-FEB-1995)
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181 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC 240
185 VQPPSSGIYSATYLEASPLGSAFFRLIVRGCGAGRWGPGCTKECPGCLHGGVCHDHDGEC 244
 65 MNQHQDPLEVTQDVTREWAKKVVWKR-EKASKINGAYFCEGRVRGEAIRIRTMKMRQQAS 123
 | : : | : : | STPPGPPLR----LARNGSHQVTLRGFSKPSDLVGVFSCVGGAGARRITRVIYVHNSPGAH 126
 FLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPD---ILEVHLPH 180
 | |: | |: | | |: : | | | : : | | | |: : : | | | |: : : | | | |: : : | | | |: : : | | | |: : : | | | |: : : | | | |: : : | | | |: : : | | | |: : : | | |: : : | | |: : : | | |: : : | |: : | | |: : : | |: : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : |: : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : |: : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |:
 14 LLLSGTVEGAMDLILINSLPLVSDAETSLTCI-----ASGWRPHEPITIGRDFEAL 64
 Query Match 42.0%; Score 2527; DB 1; Length 1138;
Best Local Similarity 46.7%; Pred. No. 2.7e-136;
Matches 541; Conservative 165; Mismatches 372; Indels 80; Gaps
 839 1118 Procedur Kinase.
845 853 ATP (By similarity).
879 979 Proton acceptor (By similarity).
870 ATP (By similarity).
870 ATP (By similarity).
871 ATP (By similarity).
872 ATP (By similarity).
873 N-linked (GloNAc. .) (Potential).
874 N-linked (GloNAc. .) (Potential).
875 503 N-linked (GloNAc. .) (Potential).
876 596 N-linked (GloNAc. .) (Potential).
877 N-linked (GloNAc. .) (Potential).
878 S96 N-linked (GloNAc. .) (Potential).
879 709 N-linked (GloNAc. .) (Potential).
870 709 N-linked (GloNAc. .) (Potential).
871 AND N-linked (GloNAc. .) (Potential).
872 709 N-linked (GloNAc. .) (Potential).
 Cytoplasmic (Potential).
Ig-like C2-type 1.
EGF-like 1.
EGF-like 2.
 Fibronectin type-III 1. Fibronectin type-III 2. Fibronectin type-III 3.
 Ig-like C2-type 2.
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 R RIMITS; PRO0109; TYRKINASE.

R RODOM; PD000001; Prot_kinase; 1.

R ROMART; SM00109; IG; 2.

SMART; SM00109; IG; 1.

SMART; SM00109; IG; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

R ROSITE; PS00022; EGF 2; 3.

R RPGSITE; PS50026; EGF 3; 2.

R ROSITE; PS50010; PROTEIN KINASE DOW; 1.

R ROSITE; PS50011; PROTEIN KINASE DOW; 1.

R ROSITE; PS001019; PROTEIN KINASE DOW; 1.

R ROSITE; PS00109; PROTEIN KINASE TYR; 1.

R ROSITE; PS00109; PROTEIN KINASE TYR; 1.

R ROSITE; PS00109; PROTEIN KINASE TYR; 1.

R ROSITE; PS00109; PROTEIN KINASE TYR; 1.

R RECEPTOR; Repeat; Signal; Nucleotide-binding; Phosphorylation; Mrinase; Miltigene family; Nucleotide-binding; Phosphorylation; Tyrosine-protein kinase.

Tyrosine-protein kinase.

T SIGNAL 1.
 Tyrosine-protein kinase receptor Tie-1
Tyrosine-protein kinase receptor Tie-1 precursor (EC 2.7.1.112).

Name-TTE1; Synonyms-TIE, TIE-1;
Bos taurus (Bovine).

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurusaiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Bovinae; Bos.

 eubfamily.
 -!- SIMILARITY: Contains 3 EGF-like domains.
 -!- SIMILARITY: Contains 3 fibronectin type-III domains.
 -!- SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like) domains.

 -1- SIMILARITY: Belongs to the Tyr protein kinase family. Tie
 Extracellular (Potential)
Potential.
Cytoplasmic (Potential).
 Ig-like C2-type 1.
EGF-like 1.
 EMBL; X71423; CAA50554.1; -; mRNA. PIR, S57845; S57845.
HSSP, Q02763; IPVR.
SMR; Q06605; B26-1134.
InterPro; IPR000742; EGF 1; InterPro; IPR005709; EGF 1ike.
InterPro; IPR005109; EGF 1ike.
InterPro; IPR005109; IPGF.
InterPro; IPR001519; IGF.
InterPro; IPR00110; IG-1ike.
InterPro; IPR00110; IG-1ike.
InterPro; IPR00110; IG-1ike.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase AS. Pfam; PF00041; ffa; 3.
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TRANSMEM
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 536 FTTASIGLPPPRGLNLLP-----KSOTTLNLTWQ--PI-FPSSEDDFYVEVERRSVQK 585
 693
 DVKIKNAŢIIQYQLKGLEPEŢAYQVDIFA-----ENNIGSSNPAFSHELVTLPESQA 737
 72
 16 LSGTVEGAMDLILINSLPLVSDAETSLTCI-----ASGWRPHEPITIGRDFEALMN
 67 QH--QDPLEVTQDVTREWAKKVVWKR-EKASKINGAYFCEGRVRGEAIRIRTMKMRQQAS
 73 PRPWQPP----HIARNGSSRVTVRGFSQPSDLVGVFSCVG---GGGTRVLYYHNSPGAH
 124 FLPATLTMTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPD---ILEVHLPH
 181 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 241 ICPPGFMGRTCEXACELHTFGRTCKERCSGOEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 301 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE
 303 ACAPGRFGADCHLQCQCQNGGTCDRFSGCVCPSGWHGMHCEKSD---RIPQILDMVSELB
 361 VNSGKFNPI-CKASGWPLPTNBEMTLVKPDGTV-LHPKDFNHTDHFSVAIFTIHRILPPD
 360 FNLDTMPRINCAAAGNPFPVRGSMELRKPDGTVLLSTKAIVEPDR-TTAEFEVPRLALGD
 SGVWVCSVNTVACMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVIN--ISSBPYFGDGPI
 477 KSKKLLYKPVNHYBAWQHIQV-TNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRR
 586 SDQQNIKVPGNLTSVLLNNLHPREQYVV-------RARVNTKAQGEWSEDLT
 590 ERRENVSSPOARTA-LLTGLTPGTYYOLDVRLYHCTLLGPASPAARVLLPPSG----
 531 AWTLSDILPPQPENIKISNITHSSAVISWTILDGYS--ISSITIRYKVQGKNED---QHV
 (By
301 EGF-like 2.
343 IGF-like 3.
424 IG-like C2-type 2.
535 Fibronectin type-III 1.
635 Fibronectin type-III 2.
734 Protein kinase.
851 ATP (By similarity).
868 ATP (By similarity).
868 ATP (By similarity).
868 ATP (By similarity).
869 ATP (By similarity).
860 ATP (By similarity).
861 ATP (By similarity).
862 ATP (By similarity).
863 ATP (By similarity).
864 N-linked (GlCNAc. ..) (Potential).
865 N-linked (GlCNAc. ..) (Potential).
866 N-linked (GlCNAc. ..) (Potential).
867 N-linked (GlCNAc. ..) (Potential).
868 N-linked (GlCNAc. ..) (Potential).
869 N-linked (GlCNAc. ..) (Potential).
860 N-linked (GlCNAc. ..) (Potential).
870 N-linked (GlCNAc. ..) (Potential).
870 N-linked (GlCNAc. ..) (Potential).
 Query Match 42.0%; Score 2526; DB 1; Length 1136; Best Local Similarity 46.4%; Pred. No. 3.1e-136; Matches 541; Conservative 159; Mismatches 363; Indels 104;
 ••
 1136 AA;
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 TPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRML 1096
 STRAIN-CSTBL/60; TISSUE-Heart, and Lung;

MEDLINE-21085660; PubMed=11217851; DOI=10.1038/3505500;

A Arakawa T. Shinagawa A.; Shibata K., Yoshino M.; Itoh M.; Ishii Y.,

A Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,

Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Pujita M., Gariboldi M.,

Byons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
DRPEETSTIV----RGLNASTRYLFRVRASVQGPGDWSNVVEQSTLGNGLQIEGPVQEIH 749
 856
 PADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQN-VREPAVOF
 MKEYASKODHRDFAGELBVLCKLGHHPNI INLLGACEHRGYLYLAI EYAPHGNLLDFLRK
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 NSGTLALNRKVKNNPDPT1YPVLDWND1KFQDVIGEGNFGQVLKAR1KKDGLRMDAA1KR
 SRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENY
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
Muridae; Murinae; Mus.
 STRAIN=C57BL/6J; TISSUE=Heart, and Lung;
MEDLINE=9927923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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01-MAR-2003 (TrEMBLrel. 23, Created)
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01-PEB-2005 (TrEMBLrel. 29, Last annotation update)
Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched
library, clone:D330005P09 product:tyrosine kinase receptor 1, full
insert sequence (Mus musculus 13 days embryo lung cDNA, RIKEN full-
length enriched library, clone:D430008P04 product:tyrosine kinase
 PRT; 1134 AA.
 1097 EERKTYVNTTLYEKFTYAGIDCSAEEA 1123
 EARKAYVNMSLFENFTYAGIDATAEEA 1136
 Meth. Enzymol. 303:19-44(1999).
 QBBGIZ MOUSE PRELIMINARY,
 Mus musculus (Mouse)
 NUCLEOTIDE SEQUENCE
 NUCLEOTIDE SEQUENCE
 NCBI TaxID=10090;
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STRAIN-C57BL/61; TISSUE-Heart, and Lung;

WEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

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 NUCLEOTIDE SEQUENCE
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 109 ARRTRVLYVHNSPGAHLFPDKVTHTVNKGDTAVLSAHVHKEKQTDVIWKNNGSYFNTLDW 168
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 108 GEAIRIRTMKWRQQASFLPATLTWTVDKGDNVNISFKKVLIKEEDAVIYKNGSFIHSVPR 167
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 347 RMTPKIVDLPDHIEVNSGKFNPI-CKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFS 405
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 63
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Saaaki D. Shibadata K., Shinagawa A., Shizaki T., Soagabe Y., Tagami M., Tagawa A., Takahasah E., Takakalira S., Takada Y., Tagami M., Tagawa A., Takahasah E., Takakalira S., Takada Y., Tagami M., Tagawa A., Toya T., Yasunishi A., Muramateu M., Hayashizaki Y., Tagami M., Mushi, Ako52192; BAC34976.1; -; mRNA.

B MBL, Ako52192; BAC34976.1; -; mRNA.

B MBL, Ako52192; BAC34976.1; -; mRNA.

B MBL, Ako52192; BAC34976.1; -; mRNA.

B MG1:9906 Tiel.

B MG1:9906 Tiel.

B MG1:9906 Tiel.

GO; GO:0016615; C:atracacllular space; TAS.

GO; GO:0016515; C:atracacllular space; TAS.

GO; GO:0010316; P:negative regulation of angiogenesis; IMP.

GO; GO:0010316; P:negative regulation of angiogenesis; IMP.

GO; GO:0010316; P:negative regulation of angiogenesis; IMP.

GO; GO:0010316; P:negative regulation of angiogenesis; IMP.

GO; GO:0010316; P:negative regulation of angiogenesis; IMP.

GO; GO:0010316; PRO00329; IEGF 1.

BR InterPro; IPR001369; PROII.

BR InterPro; IPR001369; PROII.

BR InterPro; IPR001399; IGF.

BR InterPro; IPR001399; IGF.

BR InterPro; IPR001399; IGF.

BR InterPro; IPR001399; IGF.

BR InterPro; IPR00109; Prott kinase.

BR InterPro; IPR00109; IGF.

BR PR00118; BR00119; EGF.

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 5 ASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIA----SGWRPHEPITIGRD
 Query Match 41.9%; Score 2521; DB 2; Length 1134; Best Local Similarity 45.7%; Pred. No. 6e-136; Matches 541; Conservative 158; Mismatches 364; Indels 122;
 1134 AA; 124582 MW; 9669098A843B36F2 CRC64;
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 636 PPSG-------PPAPRHLHAQALSDSEIQLMWQHPEAPSGPISKYIVEIQVA
465 -ISSEPYFGDGPIKSKKLLYKPVNHYEAWQHIQV-TNEIVTLNYLEPRTEYELCVQLVRR
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 678 GKNED-QHVDVKIKNATIIQYQLKGLEPETAYQVDIFAE-------NNIG
 SEGP-----VRESRA-AEBGLDQQLVLAVGSVSATCLTILAALLALVCIRRSCLHR
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Sequence

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Result

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 Indele
 COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/323,474
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US-08-431-922A-12
US-08-431-922A-12
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US-08-431-92
US-09-620-561-2
US-09-383-630-3
US-08-451-473E-25
US-09-862-027-25
 Sequence 2, Application US/08323474

Sequence 2, Application US/08323474

Parent No. 5447604

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Parent No. 5447607

Parent No. 5447607

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation
STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US
 h similarity 100.0%; Score 6013; Similarity 100.0%; Pred. No. 0; 24; Conservative 0; Mismatches
 ALIGNMENTS
 CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,600
PLING DATE: 26-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2609
TELECHONICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: 756822
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1124 amino acids
 Query Match 100.
Best Local Similarity 100.
Matches 1124; Conservative
 MOLECULE TYPE: protein
 amino acid
 linear
 98101
 TOPOLOGY:
 US-08-323-474-2
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7769, Ap
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 96, Appl
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 March 14, 2006, 01:48:13 ; Search time 50 Seconds (without alignments) 1858.549 Million cell updates/sec
 Sequence 2, Appli
 Sequence 22, Appl
Sequence 3, Appli
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 Issued Patents AA:*

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US-09-733-764-2
 US-08-323-474-3
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 Post-processing: Minimum Match 0%
Maximum Match 100%
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100.0%; Score 6013;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1124; Conservative 0; Mismatches
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Patent No. 6812339
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US-09-949-016-5946
 US-09-949-016-5946
 SEQ ID NO 5946
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GENERAL INFORMATION:
GENERAL INFORMATION:
TELLIGANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION NUMBER: USO9/949,016
CURRENT APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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 APPLICANT: Breitman, Martin L.
APPLICANT: Rossant, Janet
APPLICANT: Dumont, Daniel J.
APPLICANT: Yamaguchi, Terry P.
TITLE OF INVENTION: No. 5681714el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 33
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 ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 372
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,089A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 530
 Sequence 6, Application US/08278089A Patent No. 5681714 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M.
 CORRESPONDENCE ADDRESS: ADDRESSEE: Bereskin
 RESULT 5
US-08-278-089A-6
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 FAUCHING NO. 9011339;
FAUCHING NO. 9011339;
FAUCHING NO. POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO130;
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20;
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR PLILOTATION NUMBER: 60/241,755
PRIOR PLILOTATION NUMBER: 60/241,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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 Sequence 9568, Application US/09949016
Patent No. 6812339
 Best Local Similarity 99.9
Matches 1123, Conservative
 TYPE: PRT
ORGANISM: Human
 US-09-949-016-9568
 US-09-949-016-9568
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 43; Indels
 92.7%; Score 5575; D
92.5%; Pred. No. 0;
tive 37; Mismatches
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEPRAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 amino acids
 Best Local Similarity 92.5
Matches 1041; Conservative
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-089A-6
 amino acid
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 APPLICANT: Rossant, Janet
APPLICANT: Rossant, Janet
APPLICANT: Breitman, Martin L.
APPLICANT: Brown, Janet
APPLICANT: Dumont, Janet
APPLICANT: Vamaguchi, Terry P.
TITLE OF INVENTION: No. 5998187el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
CITY: Toronto
STRATE: Ontario
STATE: Ontario
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 SIME: ORGATIO
CONDITOR: Canada
ZIP: MSH 3Y2
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Batentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,957A
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KURTQAYK, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-212
TELEPHONE: (416) 364-7311
TELEFAX: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: AMINO ACID
 43;
 Query Match
92.7%; Score 5575; D
Best Local Similarity 92.5%; Pred. No. 0;
Matches 1041; Conservative 37; Mismatches
 ; Sequence 6, Application US/08838957A; Patent No. 5998187; GENERAL INFORMATION:
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RESULT 7 US-07-934-393B-2

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 Gaps
 8;
 Query Match 92.2%; Score 5542; DB 1; Length 1
Best Local Similarity 92.2%; Pred. No. 0;
Matches 1037; Conservative 37; Mismatches 43; Indels
 COUNTRY: ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEREDALE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PEACH IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSETPICATION NUMBER: 35
ATTORNEY/AGENT INFORMATION:
NAME: KUCÓYGK, Linda M.
REFERENCE/DOCKET NUMBER: 3153-64
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION OR SEQ 1D NO: 2:
SEQUINCE CHARACTERISTICS:
TELEFAX: (416) 354-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ 1D NO: 2:
SEQUINCE CHARACTERISTICS:
 GENERAL INFORMATION:
APPLICANT: BREITWAN, MARTIN L.
APPLICANT: BREITWAN, DANIEL
APPLICANT: DUMONT, DANIEL
APPLICANT: GRADWOHL, GERARD G.
TITLE OF INVENTION: TISSUE SPECIFIC TRANSCRIPTIONAL
TITLE OF INVENTION: REGULATORY ELEMENT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
Sequence 2, Application US/07934393B
Patent No. 5466596
 LENGTH: 1118 amino acids
 / MOLECULE TYPE: protein US-07-934-393B-2
 amino acid
 TOPOLOGY:
 301
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FILING DATE: 20-JUL-1994
CLASSIFICATION: 530
ATTORNAME: STATON: 530
NAME: KULCAÇAÇK, LİNGA M.
REGISTRATION NÜMBER: 34,971
REFERENCE/DOCKET NÜMBER: 3153-111
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFKX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 2:
TENERAL 1118 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
 , TOPOLOGY: linear
, MOLECULE TYPE: protein
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 Receptor Tyrosine Kinase
 Sequence 2, Application US/08278089A

Patent No. 5681714

GENERAL INPORMATION:
APPLICANT: Breitman, Martin L.
APPLICANT: Daniel J.
APPLICANT: Daniel J.
APPLICANT: Pamaguchi, Terry P.
TITLE OF INVENTION: No. 5681714el Receptor Tyrosine J.
CORRESPONDENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCES: Breet West
CITY: Toronto
STREET: 40 King Street West
CITY: Toronto
STARE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READBABE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,089A
 RESULT 8
US-08-278-089A-2
 421
 481
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 DB 1; Length 1118;
 43; Indels
Query Match
92.2%; Score 5542; DB
Best Local Similarity 92.2%; Pred. No. 0;
Matches 1037; Conservative 37; Mismatches
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120 120

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 DB 1; Length 1118;
 Sequence 2, Application US/08838957A
Patent No. 5998187
GENERAL INFORMATION:
APPLICANT: Breitman, Martin L.
APPLICANT: Rossant, Janet
APPLICANT: Vamaguchi, Terry P.
TITLE OF INVENTION:
NO. 5998187el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
 1074 YERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAEEAA 1118
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 Indels
 CURRENT APPLICATION: PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,957A
FILING DATE: 23-APR-1997
CLASSIFICATION: 41=
 43;
 92.2%; Score 5542; D 92.2%; Pred. No. 0; ive 37; Mismatches
 ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
STATE: Canada
ZIP: MSH 3Y2
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: Patentin Release #1.
 ATTORNEY AGENT INFORMATION:
NAME: Kurdydyk, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153
TELECOMMUNICATION INFORMATION:
TELEFRAN: (416) 364-7311
TELEFRAN: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 1118 amino acids
nino acid
 Conservative
 ; MOLECULE TYPE: protein US-08-838-957A-2
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 Query Match
Best Local Similarity
Matches 1037; Conserv
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 TOPOLOGY:
 RESULT 9
US-08-838-957A-2
 LENGTH:
 954
 1014
 179
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 320 GEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIEVNSGKFNPICKASGWPLPT
 RESULT 11
US-09-590-656-1
Sequence 1, Application US/09590656
Sequence 1, Application US/09590656
Patent No. 6413912
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
APPLICANT: Borges, Luis G.
APPLICANT: Fanslow, III, William C.
TITLE REFERENCE: 2900-A
CURRENT APPLICATION NUMBER: US/09/590,656
CURRENT FILING DATE: 1999-06-07
PRIOR FILING DATE: 1999-06-07
 1099 RKTYVNTTLYEKFTYAGIDCSAEEAA 1124
 1076 RKTYVNTTLYEKFTYAGIDCSAEEAA 1101
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 80 REWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQQASFLPATLTMTVDKGDNV 139
 NISFKKVLIKEEDAVIYKNGSFIHSVPRHEVPDILEVHLPHAQPQDAGVYSARYIGGNLF 199
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 91.8%; Score 5518; DB 1; Length 1101; 93.3%; Pred. No. 0; tive 30; Mismatches 38; Indels 6.
 Sequence 96, Application US/08469537A
Patent No. 5843749
GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TYROSINE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSER: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
 OPERATING SYSTEM: DOS
SOFTWARE: FastESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 26-UUL-1991
ATTORNEY/AGENT INFORMATION:
 NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
 INFORMATION FOR SEQ ID NO: 96:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ Version
 SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino acids
 Query Match
Best Local Similarity 93.3
Matches 1032; Conservative
 STRANDEDNESS: unknown TOPOLOGY: unknown
 MOLECULE TYPE: protein
 amino acid
 Tarrytown
 U.S.A.
 10591
 CITY: Tar:
STATE: NY
 US-08-469-537A-96
 US-08-469-537A-96
 COUNTRY:
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us-10-633-742-8.rai

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874 REPQVYTLPPSREEMTK----NQVSL--TCLVKGFYPSDIAVEWESNGQPENNYKTTPP 926
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 67.2%; Score 4043; DB 2; Length 977; 80.8%; Pred. No. 1.6e-252; Live 34; Mismatches 76; Indels 7
 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Section 1.00 | Sect
 Best Local Similarity 80.88
Matches 782; Conservative
 926
 ORGANISM: Homo sapiens
 927 VLDSDGSF
 919 VLETDPAF
 US-09-733-764-1
 ; ORGANISM: Hc
US-09-733-764-1
 121
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 Query Match
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 Gaps
 16;
 Length 977;
 76; Indels
 67.2%; Score 4043; DB 2;
80.8%; Pred. No. 1.6e-252;
iive 34; Mismatches 76;
 Query Match 67.2%;
Best Local Similarity 80.8%;
Matches 782; Conservative
 2.0
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver.
SEQ ID NO 1
LENGTH: 977
 ; TYPE: PRT
; ORGANISM: Homo sapiens
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 Gaps
 h 43.6%; Score 2623; DB 2; Length 704; Similarity 77.1%; Pred. No. 4.5e-161; Onservative 23; Mismatches 44; Indels 82;
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 RESULT 14
US-09-733-764-2
; Sequence 2, Application US/09733764
; Patent No. 6521424
; GENERAL INFORMATION:
; APPLICANT: Cerrecti, Douglas P.; APPLICANT: Borges, Luis G.; APPLICANT: Fanalow, III, William C.; TITLE OF INVENTION: TEK ANTAGONISTS; FILE REFERENCE: 2900-4
; CURRENT APPLICATION NUMBER: US/09/733,764
; CURRENT FILING DATE: 2000-12-07
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
 522 RGEGGEGH------
 Query Match
Best Local Similarity 77.1%
Matches 501; Conservative
 ; ORGANISM: Homo sapiens
US-09-733-764-2
 SEQ ID NO 2
LENGTH: 704
241
 121
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 361
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 874 REPOVYTLPPSREEMTK----NOVSL--TCLVKGFYPSDIAVEWESNGQPENNYKTTPP 926
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 82; Gaps
 Query Match
43.6%; Score 2623; DB 2; Length 704;
Best Local Similarity 77.1%; Pred. No. 4.5e-161;
Matches 501; Conservative 23; Mismatches 44; Indels 8
 US-09-590-656-2

Sequence 2, Application US/09590656

Sequence 2, Application US/09590656

Sequence 2, Application US/09590656

Sequence 2, Application US/09590656

Sequence 2, Application US/09590656

APPLICANT: Cerretti, Douglas P.

APPLICANT: Banges, Iuis G.

APPLICANT: Fanslow, III, William C.

TITLE OF INVENTION: TEK ANTAGONISTS

FILE REFERENCE: 2900-A

CURRENT APPLICATION NUMBER: 06/07

PRIOR APPLICATION NUMBER: 06/137,889

PRIOR APPLICATION NUMBER: 60/137,889

PRIOR FILING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.0
 919 VLETDPAF 926
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927 VLDSDGSF 934
 ORGANISM: Homo sapiens
 SEQ ID NO 2
LENGTH: 704
 US-09-590-656-2
 601
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; TOPOLOGY:
; MOLECULE TYPE
US-08-220-240A-5
LENGTH:
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 301 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIE 360
 VWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGD----- 473
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 539 ASIG------LPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVE 579
 APPLICANT: Alitalo, Kari
APPLICANT: Matikainen, Marja-Terttu
APPLICANT: Partanen, Juha
APPLICANT: Partanen, Juha
APPLICANT: Partanen, Juha
APPLICANT: Makela, Tomi
APPLICANT: Makela, Tomi
APPLICANT: Monomen, Jaana
TITLE OF INVENTION: TYROSINE KINASB AND USES THEREOF
NUMBER OF SCUENCES: 5
CORRESPONDENCE ADDRESS: 5
CORRESPONDENCE ADDRESSEE: Matehall, O'Toole, Gerstein, Murray & Borun
STREET: ALL STANDENCE ADDRESSEE: Matehall, O'Toole, Gerstein, Murray & Borun
STREET: ALL STANDENCE ADDRESSEE: Matehall, O'Toole, Gerstein, Murray & Borun
STREET: ALL STANDENCE ADDRESSEE: Matehall, O'Toole, Gerstein, Murray & Borun
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/220,240A
FILING DATE: 29-MAR-1994
 REFERENCE/DOCKET NUMBER: 29151/31958
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPA: (312) 474-0448
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/F193/00006
FILING DATE: 08-JAN-1993
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/817,800
FILING DATE: 09-JAN-1992
PRICE APPLICATION NUMBER: US 08/167,453
FILING DATE: 15-DEC-1993
ATTORNEY/AGENT INFORMATION:
 CITY: Chicago
STATE: Illinois
COUNTRY: Unites States of America
ZIP: 60606-6402
 Sequence 5, Application US/08220240A
Patent No. 5955291
 NAME: Gass, David A. REGISTRATION NUMBER: 38,153
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 GENERAL INFORMATION:
 CLASSIFICATION:
 US-08-220-240A-5
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 537 TTASIGLPPPRGLNLLP-----KSQTTLNLTWQ-PIFPSS--EDDFYVEVERRSVQKS
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 700 KGLEPETAYQVDIFA------ENNIGSSNPAFSHELVTLPESQAPADLGGGKM
 706 RGLNASTRÝLFRAMRÁSIQGLGDWSNTVEESTLGNGLQÁEG----PVQESRÁ-ÁEEGLDQQ
 REKLOPEPLSYPVLEWEDITFEDLIGEGNFGQVIRAMIKKDGLKMAAAIKMLKEYASEND
 14 LLLSGTVEGAMDLILINSLPLVSDAETSLTCI-----ASGWRPHEPITIGRDFEAL
 ICPPGFMGRTCEKACELHTFGRTCKERCSGQEGCKSYVFCLPDPYGCSCATGWKGLQCNE
 361 VNSGKFNPI-CKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDS
 539 TT---DCPEPL---LQPWLEGWHVEGTDRLRVSWSLPLVPGPLVGDGFLLRLWDGTRGQE
 587 DOQNIKVPGNLTSVLLNNLHPREQYVVRARV-NTKAQGEWSEDLTAWTLSDILPPQPENI
 646 KISNITHSSAVISW---TILDGYSISSITIRYKVQGKNEDQ---HVDVKIKNATIIQYQL
 747 LLIAILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQN-VREEPAVQFNSGTLALNR
 806 KVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDD
 181 AOPODAGVYSARYIGGNLFISAFTRLIVRRCEAOKWGPECNHLCTACMNNGVCHEDIGEC
 80;
 Length 1138;
 Indels
 Query Match
42.0%; Score 2527; DB 1; 1
Best Local Similarity 46.7%; Pred. No. 1.3e-154;
Matches 541; Conservative 165; Mismatches 372;
1138 amino acids
 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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8 6 6 6 6 6 6
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¹¹⁰⁶ TLYEKFTYAGIDCSAEBA 1123 :|:| ||||||| :||| 1121 SLFENFTYAGIDATAEBA 1138

Search completed: March 14, 2006, 01:49:48 Job time : 54 secs

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US-10-223-085-82
 March 14, 2006, 01:59:33 ; Search time 177 Seconds (without alignments) 2653.334 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 US-10-633-742-8
6013
1 MDSLASLVLCGVSLLLSGTV.....TTLYEKFTYAGIDCSAEEAA 1124
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
 -10-732-923-13449
 -10-732-923-13691
-10-732-923-13434
 3-10-305-654-82
3-10-394-322A-64
3-10-211-462-147
 Total number of hits satisfying chosen parameters
 .09-815-341A-1
 US-09-733-764-2
 1867569 segs, 417829326 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
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 Scoring table:
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5732.5
5580
5413
4612.5
 4043
2652
2639.5
2623
 OM protein
 Searched:
 Database
 Run on:
 Result
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Sequence 2, Appl	Sequence 15, App	8 Seguence 18, App.	9 Sequence 29, App.	Sequence 17,	01 Sequence 101, Ap	63 Seguence 63, Appl	13 Sequence 113, App	Sequence 2, Ap	Sequence 28	Sequence		3643 Sequence 13643,	B Sequence 58, App	Sequence	5543 Sequence 45543,	Sequence 2, Appl	Sequence 28, App.
US-10-357-653-2	US-10-232-838-19	US-10-232-838-18	US-10-232-838-25	US-10-232-838-17	US-10-021-660-101	US-10-394-322A-	US-10-211-462-113	US-10-916-840-2	US-10-846-113A-28	US-10-232-838-26	US-10-116-275-137	US-10-732-923-13	US-10-664-421-56	US-10-941-635-58	US-10-450-763-45543	US-09-815-341A-2	US-10-664-421-28
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2623	2606	2567	2550.5	2544	2527	2527	2527	2527	2527	2524	2515	2451	1847	1847	1791	1703	1680
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ALIGNMENTS

RESULT 1

US-10-221-085-82

US-10-221-085-82

US-10-221-085-82

Publication NO USROOJOO0497A1

Sequence 82, Application US/10223085

Publication NO USROOJOO0497A1

APPLICANT: Berrarx, Napoleone

APPLICANT: Gerriten, Mary E.

APPLICANT: Godawik, Paul J.

APPLICANT: Godawik, Paul J.

APPLICANT: Godawik, Paul J.

APPLICANT: Godawik, Paul J.

APPLICANT: Godawik, Paul J.

APPLICANT: Watanbe, Colin K.

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APPLICANT: Watanbe, Colin K.

APPLICANTON WATANBER: US (0/219, 656

PRIOR FILING DATE: 2000-02-20

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961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1020
 1021 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKCHPQGYRLEKPLNCDDEVYDLMRQCWREKPY 1080
 61 FEALMNQHQDPLEVTQDVTREWAKKVVWKREKASKINGAYFCEGRVRGEAIRIRTMKMRQ 120
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 1 MDSLASLVLCGVSLLLSGTVEGAMDLILINSLPLVSDAETSLTCIASGWRPHEPITIGRD
 - See File Wrapper or PALM.
 APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS FILE REFERENCE: P3235P1CS
CURRENT APPLICATION NUMBER: US/10/223,084
CURRENT FILING DATE: 2002-08-16
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PRIOR PELICATION NUMBER: US 60/213, 637
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-07-20
PRIOR PLICATION NUMBER: US 60/220, 624
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
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PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220, 664
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/USO0/20710
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-02
PRIOR PLING DATE: 2000-08-03
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PRIOR PILING DATE: 2000-08-24
 Sequence 82, Application US/10223084
Publication No. US20030105011A1
GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritteen, Mary E.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
Pan, James
 Best Local Similarity 100.
Matches 1124; Conservative
 ORGANISM: Homo sapiens
 Similarity
 US-10-223-084-82
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 361 VNSGKFNPICKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSG
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 LLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS
 LLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT
 1LDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS
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 DB 4;
 100.0%; Score 6013;
100.0%; Pred. No. 0;
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Best Local Similarity 100.
Matches 1124; Conservative
; ORGANISM: Homo sapiens
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 9
 GENERAL INCORATION:

APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gedoard, Audray E.
APPLICANT: Gedoard, Paul J.
APPLICANT: Gedoard, Paul J.
APPLICANT: Gedoard, Paul J.
APPLICANT: Gedoard, Paul J.
APPLICANT: Mareters, Scot A.
APPLICANT: Mareters, Scot A.
APPLICANT: Mareters, Scot A.
APPLICANT: Wealand, Jane J. Jane J.
APPLICANT: Wealand, Jane J. Jane J.
APPLICANT: Wealand, Jane J. Jane J.
APPLICANT: Wealand, Jane J. Jane J. Jane J.
APPLICANT: Wealand, Jane J.
 AQPQDAGVYSARY IGGNLPTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
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Sequence 82, Application US/10223088
Publication No. US20030105012A1
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
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 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPINCDDEVYDLMRQCWREKPY 1080
 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLFVRWMAIESLNYSVYTTNSD 1020
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 Sequence 82, Application US/10223090; Publication No. US20030105013A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Perrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Austrant: APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
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APPLICANT: Pan, Jamelerle Scot A.
APPLICANT: Stephan, Jean-Philippe F.
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APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
TITLE OF INVENTION NUMBER: US /10/223,090
TITLE OF INVENTION NUMBER: US 60/213,637
PRIOR PELING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR PELING DATE: 2000-07-26
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PRIOR PELING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,644
PRIOR APPLICATION NUMBER: US 60/220,635
PRIOR APPLICATION NUMBER: US 60/222,695
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 Length 1124;
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 DB 4;
 Query Match
100.0%; Score 6013;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1124; Conservative 0; Mismatches
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NEW PELLING DATE: 2000-00-10-30

OR PELLING DATE: 2000-06-23

OR APPLICATION NUMBER: US 60/219,556

OR FILING DATE: 2000-07-20

OR APPLICATION NUMBER: US 60/220,664

OR PILING DATE: 2000-07-25

OR APPLICATION NUMBER: US 60/220,664

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OR PILING DATE: 2000-07-28

OR APPLICATION NUMBER: US 60/22,695

OR PILING DATE: 2000-08-17

OR APPLICATION NUMBER: US 60/23,978

OR PILING DATE: 2000-08-17

OR APPLICATION NUMBER: US 60/23,978

OR PILING DATE: 2000-09-15

OR APPLICATION NUMBER: US 60/23,978

OR PILING DATE: 2000-09-16

OR APPLICATION NUMBER: US 60/23,978

OR PILING DATE: 2000-09-18

OR APPLICATION NUMBER: US 99/66,100

OR APPLICATION NUMBER: US 99/66,309

OR PILING DATE: 2000-09-18

OR APPLICATION NUMBER: US 99/66,309

OR PILING DATE: 2000-09-18

OR APPLICATION NUMBER: US 99/66,309

OR PILING DATE: 2000-11-08

OR APPLICATION NUMBER: US 99/66,400

OR APPLICATION NUMBER: US 99/66,400

OR APPLICATION NUMBER: US 99/709,238

OR FILING DATE: 2000-11-08

OR APPLICATION NUMBER: US 99/70,709

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OR APPLICATION NUMBER: US 99/80,498

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OR APPLICATION NUMBER: US 99/80,498

OR PILING DATE: 2001-01-22

OR APPLICATION NUMBER: US 99/80,498

OR PILING DATE: 2001-01-22

OR APPLICATION NUMBER: US 99/80,699

OR PILING DATE: 2001-03-28

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OR PILING DATE: 2001-03-38

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OR PILING DATE: 2001-03-09

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OR APPLICATION NUMBE OR FILING DATE: 2001-05-10
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OR FILING DATE: 2001-05-25
OR APPLICATION NUMBER: PCT/US01/17092
OR APPLICATION NUMBER: US 09/870,574
OR FILING DATE: 2001-05-30 RANGER BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BRIGGE BR IHRDLAARNIIVGENYVAKIADFGLSRGGEVYVKKTMGRLPVRMMAIESLNYSVYTTNSD 1020 961 IHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSD 1020 1021 VWSYGVLLWEIVSLGGTPYCGMTCAELYEKTPQGYRLEKPINCDDEVYDLMRQCWREKPY 1080 VWSYGVILWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPY 1080 540 909 601 LLANLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT 660 720 720 780 780 MAQAFQNVREBPAVQFNSGTLALNRKVKNNPDPTIYPVLDWNDIKFQDVIGEGNFGQVLK 840 840 ARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYL 900 AIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQF 960 SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR AIEYAPHGNILDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQQQF LLYKPVNHYBAWQHIQVTNBIVTLNYLBPRTBYBLCVQLVRRGEGGGGGHPGPVRRFTTAS ILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGS SNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRR LLYKPVNHYBAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRFTTAS LINNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWT

APPLICATION NUMBER: PCT/US01/17443 FILING DATE: 2001-05-30 APPLICATION NUMBER: PCT/US01/17800

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 APPLICANT: Mareteres, Scot A.
APPLICANT: Far, James
APPLICANT: Stephan, Jean-Philippe F.
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APPLICANT: Watenabe, Colin K.
APPLICANT: Wood, William I.
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APPLICANT: We, Weiliam P. Mickey
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APPLICANTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
CURRENT APPLICATION NUMBER: US 10/081,056
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PLING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,644
PRIOR PILING DATE: 2000-07-25
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 Sequence 82, Application US/10223083
Publication No. US20030119112A1
 APPLICANT: Baker, Kevin P.
APPLICANT: Berrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerriteen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
 TYPE: PRT
ORGANISM: Homo sapiens
 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-06-39
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APPLICANT: Gerber, Hary E.
APPLICANT: Gerber, Hary E.
APPLICANT: Goddard, Audrin L.
APPLICANT: Goddard, Audrin L.
APPLICANT: Goddard, Audrin L.
APPLICANT: Goddard, Audrin L.
APPLICANT: Goddard, Audrin L.
APPLICANT: Goddard, Audrin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: MAILAIN, Kenneth J.
APPLICANT: Wellam I.
APPLICANT: Wellam I.
APPLICANT: Willam, P. Mickey
APPLICANT: Willam, P. Mickey
APPLICANT: Wellam I.
APPLICANT: Willam, P. Mickey
APPLICANT: Willam, P. Mickey
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APPLICANT: Wold, Willam, P. Mickey
APPLICANT: Wold, Willam, P. Mickey
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PRIOR PRILING PAPELICATION NUMBER: PCT/US00/23328
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 APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertiteen, Mary E.
APPLICANT: Godward, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
 US-10-223-089-82
; Sequence 82, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
 Best Local Similarity 100.
Matches 1124; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-089-82
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 SEC ID NO 82
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APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Gorgonia Susan No. US20030152956Alel Methods of Diagnosis of Angiogenesis
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Modulators
FILE REFERENCE: 018501-00710US
CURRENT APPLICATION NUMBER: US/09/784,356
PRIOR APPLICATION NUMBER: US/09/784,356
PRIOR PLING DATE: 2001-02-14
PRIOR PLING DATE: 2000-08-11
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ative 0; Mismatches
Sequence 112, Application US/10021660
Publication No. US20030152926A1
GENERAL INFORMATION:
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 US-10-021-660-112
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PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See File Wrapper or PALM.
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 ; ORGANISM: Homo sapiens
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Sequence 82, Application US/1023081

Sequence 82, Application US/1023081

SEQUENCE 82, Application US/1023081

SEQUENCE 82, Vevin P.

APPLICANT: Baker, Kevin P.

APPLICANT: Garitsen, Mary E.

APPLICANT: Garitsen, Mary E.

APPLICANT: Godowski, Paul J.

APPLICANT: Glarney, Marthn L.

APPLICANT: Glarney, Marthn L.

APPLICANT: Hangeter Scot A.

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APPLICANT: Marters, Scot A.

APPLICANT: Marters, Scot A.

APPLICANT: Marters, Dames

APPLICANT: Marters, Dames

APPLICANT: We manha, Colin K.

APPLICANT: We stand I.

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BRIOR PILING DATE: 2000-07-28

PRIOR APPLICANTION NUMBER: US 60/220,664

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 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Berrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Mary E.
APPLICANT: Geddard, Audrey
APPLICANT: Goddwski, Paul J.
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APPLICANT: Hillan, Kenneth J.
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APPLICANT: Pan, J.
APPLICANT: Pan, J.
APPLICANT: Reanabe, C.K.
APPLICANT: Wood, W.I.
APPLICANT: Wellan
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
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CURRENT PILING DATE: 2002-11-26
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100.0%; Pred. No. 0;
tive 0; Mismatches
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ORGANISM: Homosapiens
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WS-10-211-462-147

Sequence 147, Application US/10211462

Publication No. US20040033495A1

Sequence 147, Application US/10211462

Publication No. US200400333495A1

APPLICANT: Murray, Richard

APPLICANT: Matesn, Susan R.

APPLICANT: Matesn, Susan R.

APPLICANT: Matesn, Susan R.

APPLICANT: Matesn, Susan R.

APPLICANT: Matesn, Susan R.

TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis Modulators

TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis Modulators

FILE REFERENCE: 018501-006200US

CURRENT PILING DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: US 60/310,025

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PRIOR FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 230

SOFTWARE: Patentin Ver. 2.1

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DR FILING DATE: 2001-05-30
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 TATION NUMBER: PCT/USO0/23522

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R APPLICATION NUMBER: PCT/USO0/23328

R RILING DATE: 2000-08-24

R APPLICATION NUMBER: US 60/230,978

R RILING DATE: 2000-09-07

R FILING DATE: 2000-09-07

R FILING DATE: 2000-09-15

R FILING DATE: 2000-09-15

R APPLICATION NUMBER: US 60/664,610

R FILING DATE: 2000-09-18

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 FILING DATE: 2000-07-28
APPLICATION NUMBER: US 60/222,695
 LING DATE: 2001-06-01
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 APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: COMPOSITIONS AND DISORDERS INVOLVING ANGIOGENESIS
FILE REPERENCE: P23.35-PIC.
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR PILING DATE: 2001-07-09
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 Stephan, Jean-Philippe F. Watanabe, Colin K. Wood, William I. Williams, P.Mickey
 Sequence 82, Application US/10081056 Publication No. US20040043927A1 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerriteen, Mary E.
APPLICANT: Gerriteen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
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APPLICANT: Hillan, Kenneth J.
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; Publication No. US20050158771A1
; GENERAL INFORMATION:
; APPLICATION:
; TITLE OF INVENTION: novel targets for obesity fro
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; CURRENT FILING DATE: 2004-12-22
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LOCATION: (1). (1124)
OTHER INFORMATION: LocusID: 7010
OTHER INFORMATION: NM_000459
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US-11-019-855-47
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LENGTH: 1124
 US-11-019-855-47
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 TYPE: PRT
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4 4 4 4 4 4 4 4 4 4 1 1 1 1 1 1 1 1 1 1	601 601 661	721 721 781	841 841 901	961 961 1021 1021	1081
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 SEQ ID NO 162
LENGTH: 1124
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 1622, Ap
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4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
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5.1.7
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US-11-093-146-75
US-11-092-168-9
US-11-113-424-61
US-11-113-424-61
US-11-17-894-17
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US-11-17-894-16
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US-10-821-234-1587
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US-10-511-273-1
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version = 2006 E
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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Match Length
 Title:
Perfect score:
 Scoring table:
 OM protein
 Minimum DB
Maximum DB
 Sequence:
 Database
 Run on:
 Result
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JOS-LIT OF 27-25-26.

PUBLICATION NO. US20060024297A1

GENERAL INFORMATION:

APPLICANT: Wood, Clive R.

APPLICANT: Pieters, Henk

APPLICANT: Pieters, Henk

APPLICANT: Hotch, Simon E.

ITLE OF INVENTION: TIB COMPLEX BINDING PROTEINS

FILE REFERENCE: 10280-128001

CURRENT FILING DATE: 2005-02-02

FRIOR PILING DATE: 2005-02-02

PRIOR PLING DATE: 2004-08-12

PRIOR PLING DATE: 2004-08-12

PRIOR FILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-12

NUMBER OF SEQ ID NOS: 721

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 Sequence 2, Application US/11049536
Publication No. US20060024297A1
GENERAL INFORMATION:
APPLICANT: Wood, Clive R.
APPLICANT: Pieters, Henk
APPLICANT: Hoft, Rene
APPLICANT: Hiton, Simon E.
TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
FILLE REPERENCE: 10290-128001
CURRENT APPLICATION NUMBER: US/11/049,536
CURRENT FILING DATE: 2005-02-02
 US-11-049-536-2
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 14 LLLSGTVEGAMDLILINSLPLVSDAETSLTCI-----ASGWRPHEPITIGRDFEAL
 | |: | |: | | |: : | | | |: : | | | |: : | | | |: : : | | |: : : | | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : | |: : : | |: : : | |: : | |: : | |: : : | |: : | |: : | |: : | |: : | |: : | |: : | |: : | |: | |: : | |: | |: : | |: | |: : | |: | |: : | |: | |: : | |: | |: | |: : | |: | |: : | |: | |: : | |: | |: : | |: | |: | |: : | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |: | |:
 65 MNOHODPLEVTODVTREWAKKVVWKR-EKASKINGAYFCEGRVRGEAIRIRTMKMROOAS
 | | : | : | | : | | : | | | : | | RTPPGPPLR----LARNGSHQVTLRGFSKPSDLVGVFSCVGGAGARRTRVIYVHNSPGAH
 185 VQPPSSGIYSATYLEASPLGSAFFKLIVRGCGAGRWGPGCTKECPGCLHGGVCHDHDGEC
 301 ACHPGFYGPDCKLRCSCNNGEMCDRFQGCLCSPGWQGLQCEREGIPRMTPKIVDLPDHIB
 SKKLLYKPVNHYBAWQHIQV-TNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRRF
 539 Tr---DCPEPL---LOPWLEGWHYEGTDRLRVSWSLPLVPGPLVGDGFLLRLWDGTRGQE
 700 KGLEPETAYQVDIFA------ENNIGSSNPAFSHELVTLPESQAPADLGGGKM
 241 ICPPGFMGRICEKACELHIFGRICKERCSGQEGCKSYVFCLPDPYGCSCAIGWKGLQCNE
 362 FNLETMPRINCAAAGNPFPVRGSIELRKPDGTVLLSTKAIVEPEKTTAEFEVPRLVLADS
 DOONIKVPGNLTSVLLNNLHPREQYVVRARV-NTKAQGEWSEDLTAWTLSDILPPQPENI
 LLIAILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQN-VREEPAVQFNSGTLALNR
 AQPQDAGVYSARYIGGNLFTSAFTRLIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGEC
 361 VNSGKFNPI-CKASGWPLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDS
 TTASIGLPPPRGLNLLP-----KSQTTLNLTWQ-PIFPSS--EDDFYVEVERRSVQKS
 KISNITHSSAVISW---TILDGYSISSITIRYKVQGKNEDQ---HVDVKIKNATIIQYQL
 Gaps
 80;
 Length 1138
 Indels
 Query Match 42.0%; Score 2527; DB 7;
Best Local Similarity 46.7%; Pred. No. 1.1e-162;
Matches 541; Conservative 165; Mismatches 372;
PRIOR APPLICATION NUMBER: US 10/916,840
PRIOR FILING DATE: 2004-08-12
PRIOR APPLICATION NUMBER: US 60/494,713
PRIOR FILING DATE: 2003-08-12
NUMBER OF SEQ ID NOS: 721
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
```

:    :      :	: :
Qy 866 HRDFAGELEVLCKLGHHPNIINLGACEHRCYLYLAIEYAEHGNLLDFLRKSRVLETDPA 925 	Qy 685 VDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIG-SSNPAFSHELVTLPESQAPADLGG 743 ::
Qy 926 PAIANSTASTLSSQQLLHFAADVARGWDYLSQKQFIHRDLAARNILVGENYVAKIADFGL 985    :	OY 744 GKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRRWAQAFQNVR 789 :
Qy 986 SRGQEVYVKKTMGRLEVRWMAIESLNYSVYTTNSDVMSYGVLLMEIVSLGGTPYCGMTCA 1045	QY 790 BEPAVQFNSGTLALNRKVKNNNPDPTIYPVLDWNDIKFQDVIGEGNF 835
QY 1046 BLYEKLPQGYRLEKPLNCDDEVYDLWRQCWREKPYERPSFAQILVSLNYMLEERKTYVNT 1105	QY 836 GQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINL 888
Qy         1106 TLYEKFTYAGIDCSAEEA 1123           bb         1121 SLFENFTYAGIDATAEEA 1138	QY 889 IGACEHRGYLYLAIEYAPHGNILDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADV 948
RESULT 3 US-11-183-567A-2 ; Sequence 2, Application US/11183567A ; Publication No. US20060019295A1	OY 949 ARGMDYLSOKOFIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWM 1005
. INFORMATION: SANT: Zhou, Ming-Ming SANT: Goldfarb, Mitchell	899
; TITLE OF INVENTION: Methods of Identifying Modulators of the ; TITLE OF INVENTION: FOR Receptor ; FILE REFERENCE: 2459-1-002NCON ; CURRENT APPLICATION NUMBER: US/11/183,567A	Qy 1066 EVYDLARQCWREKPYERPSFAQILVSLARMLEERKTYVNTTL 1107 
; CURRENT FILING DATE: 2005-07-18 ; PRIOR APPLICATION NUMBER: 09/757,415 ; PRIOR FILING DATE: 2001-01-09 ; PRIOR APPLICATION NUMBER: 60/175,867 ; PRIOR PILING DATE: 2000-01-12	RESULT 4 US-11-072-175-254 ; Sequence 254, Application US/11072175 ; Publication No. US20060029944A1
; NUMBER OF SEQ ID NOS: 33 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2 ; LENGTH: 822	; GENERAL INFORMATION: ; APPLICANT: Bristol-Myers Squibb Company ; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT ; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TYPE: PRT ; ORGANISM: Mus musculus US-11-183-567A-2	; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS ; FILE REPERRICE: D0273A CIP ; CURRENT APPLICATION NUMBER: US/11/072,175  — CHRENT PATTING DAME: 306-03.06
Query Match Best Local Similarity 27.4%; Pred. No. 3.1e-39; Matches 226; Conservative 132; Mismatches 297; Indels 169; Gaps 24;	FRIOR APPLICATION NUMBER: US 60/406,385 FRIOR FILING DATE: 2002-08-27 FRIOR FILING DATE: 2002-08-27 FRIOR PRICATION NUMBER: US 10/648,593
Qy 371 KASGWPLPTNEEMTLVKP	; FYCOK FILING DATE: 2003-20; NUMBER OF SEQ 1D NOS: 571; SOFTWARE: Patentin version 3.2; SOFTWARE: Patentin version 3.2; FYCOK TOWNS 10 NO 554
Qy 410 TIHRILPPDSGVWVCSVNTVAGMVEKPFNISVK-VLPKPLNAPNVIDTGHNFAVINISSE 468 : :         : :       :	; TYPE: PRT ; TYPE: PRT ; ORGANISM: Homo sapiens US-11-072-175-254
QY 469 PYFGDGPIKSKGLYKPVNHYBAWQHIQVTNBIVTLNYLEPRTEYBLCVQLVRRGEGGEG 528  138 EKETDNTKPNRRPVAPYWTSPEKMEKGLHAVPAAKTVKFKCPSSG 182	Query Match Best Local Similarity 27.7%; Pred. No. 1.18-36; Matches 214; Conservative 140; Mismatches 293; Indels 126; Gaps 24;
Qy 529 HPGPVRRFTTASIGLPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKS 586	QY 381 EEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSGVWVCSVNTVAGMVEK 435
Qy 587 DQQNIKVPGNLISVLLMNLHPREQYVVRARVNTKAQGE 624   ::	Qy 436 PFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKKLLYKPVNHYBAWQ 493
625 WSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILDGYSISSITIRYKVQGKNEDQH	494

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SEQ ID NO 75
LENGTH: 258
 US-11-092-168-9
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 987 R---GQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMT 1043
 590 DINRVPEEQMTFKDLVSCTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGLA 649
224 SDKGNYTCVVENEYGSINHTYHLDVVERSPHRPILQ-AGLPANASTVVGGDVEFVCKVYS 282
 NLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILD 663
 283 DAQPHIQWIKHVEKNGSKYG------ 324
 664 GYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGSSNP 723
 325 -LALFNVT-----VSNYIGQANQ 351
 724 AFSHELVTLPESQAPA---DLGGGKMLLIAILGSAGMTCLTVLLAFLIILQLKRA---- 775
 352 --SAWLTVLPKQQAPGREKEITASPDYLEIAIYCIGVFLIACMVVTVILCRMKNTTKKPD 409
 776 -----NVQRRMAQAFQ-NVREEPAVQFNSGT--LALNRKVKNNPD-PIIYPVLDW-- 821
 822 -NDIKFQ------DVIGEGNFGQVLKAR---IKKDGLR--MDAAIKRMKEYASKDDH 866
 867 RDFAGELEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAF 926
 530 SDLVSEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRARRPPGMEYSY 589
 927 AIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLS 986
 650 RDINNIDYYKKTTNGRLPVKMMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSBYPGIP 709
 APPLICANT: SMILENOUS STEERINGS
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Gucher. Erik
APPLICANT: Glorse, William M
APPLICANT: Glorse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Lepley, Denise M
APPLICANT: Redigaru, Muralidhara
APPLICANT: Spytek, Rimberly A
APPLICANT: Spytek, Rimberly A
APPLICANT: Shimkets Richard A
APPLICANT: Shimkets Richard A
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 2140-2124
 1044 CAELYEKLPOGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRML 1096
 710 VEELFKLIKEGHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIL 762
 554 KSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSV----
 CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR FILING DATE: 2000-09-27
 Sequence 75, Application US/10877346
Publication No. US20060014153A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Mithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
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1006 AIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDD 1065
 949 ARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSR---GQEVYVKKTMGRLPVRWM 1005
 830 IGEGNFGQVLKARIK-KDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINL 898
 889 LGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADV 948
 112 ARGMEYLESKOFVHRDLAARNCLVGENKTVKIADFGLARDLYDDDYYRKKKSPRLPIRWM 171
 APPLICANT: Arizona Board of Regents on behalf of The University of Arizona APPLICANT: Montigen Pharmaceuticals, Inc.
APPLICANT: Hurley, Laurence H.
APPLICANT: Mahadevan, Daruka
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR PILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR FILING DATE: 2000-09-28
PRIOR PILING DATE: 2000-10-28
PRIOR PILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
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PRIOR PILING DATE: 2000-10-05
 Query Match 10.8%; Score 646.5; DB 6; Length 258;
Best Local Similarity 49.4%; Pred. No. 1.6e-36;
Matches 132; Conservative 40; Mismatches 76; Indels 19; Gaps
 OTHER INFORMATION: Description of Artificial Sequence: Tyrosine OTHER INFORMATION: Kinase Consensus Sequence
 APPLICANT: Della Croce, Kimiko
APPLICANT: Von Hoff, Daniel D.
APPLICANT: Grand, Cory L.
TILE OF INVENTION: PROTEIN KINASE INHIBITORS
FILE REFERENCE: 920214.00003CONT3
 1066 EVYDLMRQCWREKPYERPSFAQILVSL 1092
 Han, Haiyong
Bearss, David J.
Vankayalapati, Hariprasad
Bashyam, Sridevi
Munoz, Ruben M.
Warner, Steven L.
Della Croce, Kimiko
Von Hoff, Daniel D.
 Sequence 9, Application US/11092168
Publication No. US20050277658A1
GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Xenopus laevis
 US-11-113-424-59
 ; OKGANISM: XE
US-11-113-424-61
SEQ ID NO 61
LENGTH: 985
 700
 817
 Query Match
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 LPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEK 1059
 3
 207 LPVKWAABBALFDRIYTHQSDVWSFGVILWEIFTLGGSPYPGVPVEELFKLLKEGHRMDK 266
 883 PNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLL 942
 29 LGEGAFGQVVLA--EAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKH
 943 HFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSRG---QEVYVKKTMGR
 830 IGEGNFGQVLKARIKXDGLRMD-----AAIKRMKEYASKDDHRDFAGELEVLCKLGHH
 Gaps
 JANUARE LINGUALION: POLYPEPTIGES and Nucleic Acids Encoding Same TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same CURRENT APPLICATION NUMBER: US/11/113,424

CURRENT PILING DATE: 2005-04-21

PRIOR PILING DATE: 2000-12-19

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-29

PRIOR PILING DATE: 2001-08-29

PRIOR PILING DATE: 2001-09-14

PRIOR PILING DATE: 2001-09-14

PRIOR PILING DATE: 2001-09-14

PRIOR PILING DATE: 2001-09-14

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-05-29

PRIOR PILING DATE: 2001-05-29

PRIOR PILING DATE: 2001-05-02

PRIOR PILING DATE: 2001-05-02

PRIOR PILING DATE: 2001-05-02

PRIOR PILING DATE: 2001-05-02

PRIOR PILING DATE: 2001-05-02
 Query Match 10.5%; Score 633; DB 7; Length 310; Best Local Similarity 46.9%; Pred. No. 1.6e-35; Matches 130; Conservative 54; Mismatches 81; Indels 12;
 PLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRML 1096
 | || :|:|:| :|| || | | :||:| |:: |::|::
PSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIV 303
 CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: US 10/965,313
US 60/608,529
US 60/511,486
US 60/511,489
PRIOR FILING DATE: 2004-10-14
2003-10-14
2003-10-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 9
SEQ ID NO 9
CURRENT APPLICATION NUMBER: US/11/092,168
 Sequence 61, Application US/11113424
Publication No. US20050260713A1
 LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-092-168-9
 GENERAL INFORMATION
 -11-113-424-61
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986 SRGQE-----VYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYC 1040
 1041 GMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERK 1100
 441
 442 TVTQIQPKEITRHSVSLTWP--EPERANGVILLEYEVKYYEKDQNERSYRIVKTASRSADI 499
 663 RRDFLSEASIMGQP-DHPNIIHLEGVVTKCKPVMIITEYMENGSLDAFLRKN----DGR 716
 641 QPENIKISNITHSSAVISWTILDGYSISSITIRYKVQGKNEDQHV-DVKIKNATIIQYQL 699
 758 TCLTVLLAFLIILQLKRANVQRRMAQAFQNVREEPAVQFNSGTLALNRKVKNNPDPTIY- 816
 ------PVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLR-MDAAIKRMKEYASKDD 865
 866 HRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPA 925
 926 FAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGL 985
 586 SDQQN-IKVPGNLTSVLLNNLHPREQYVVRA-RVN--TKAQGEWSEDLTAW-TLSDILPP
 767 SRVLEDDPEAAYTTRG-GKIPIRWTAPEAIAYRKFTSASDVWSYGIVMWEVMSYGERPYW
 386 SPOONGLKT----TKVSINDLOAHTNYTFEVWAINGVSKONPEODGAVSVTVTTNOAAPS
 KGLEPETAYQVDIFAEN - - NIGSSNPAFSHELVTLPESQAPADLGGGKMLLIAILGSAGM
 Gaps
 APPLICANT: Gangolli et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-225
CURRENT APPLICATION NUMBER: US/11/113,424
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
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PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
 96;
10.2%; Score 612; DB 7; Length 985; 29.2%; Pred. No. 2e-33;
 Best Local Similarity 29.2%; Pred. No. 2e-33;
Matches 182; Conservative 104; Mismatches 251; Indels
 544 PPPRGLNLLPK-SQTTLNLTWQPIFPSSE----DDFYVEVERR----
 1101 TYVNTTLYEKFT-YAGIDCSAEE 1122
 886 SLKRTGLENSRINTALLDPSSPE 908
 Sequence 59, Application US/11113424 Publication No. US20050260713A1 GENERAL INFORMATION:
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197

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957 OKOFIHRDLAARNILVGENYVAKIADFGLSRGOE-----VYVKKTMGRLPVRWMAIESLN 1011
 284 PYG-CSCATGW--KGLQCNEACHPGFY-GPDCKLRCS-C--NNGEMCDRFQGCLCSPGW- 335
 253 PIGKCSCNAGYEERGFWC-QACRPGFYKALDGNMKCAKCPPHSSTQEDGSMNCRCENNYF 311
 312 RADKOPPSMACTR---PPSSPRNVISNINETSVÍLDWSWPLDTGGRKDVTFNIICKKCGW 368
 376 PLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSGVWVCSVNTVAGMVEK 435
 436 PFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKKLLYKPVNHYEAWQHI 495
 388 ---- VRFLPR----- 388
 389 -LTNTTVTVTVTDLLAHTNYTFEIDAV---NGVSELSSPPROFAAVSITTNQAAPSPVLTIK 444
 KSQTTLN----LTWQPIFPSSEDDFYVEVERRRSVQKSDQQNIKVPGNLTSVLLNNLHPREQ 610
 571 TIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGSSNPAFSHELV 730
 TLPESQAPADLGG--GKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQNV 788
 789 REEPAVQFNSGTLALNRKVKNNPDPTIY------PVLDWNDIKFQDVIGEGNFGQ 837
 576 ADEKRIHFGNGHLKL-PGLRTYVDPHTYEDPTQAVHEFAKELDATNISIDKVVGAGEFGE 634
 39 DMGYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTRG-GKIPIRWTSPEAIA 797
 338 VLKARIKKDGLR-MDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRG 896
 496 QVTNEIVTLNYLEPRIEYELCVQLVRRGEGGEGHPGPVRRFTTASI--GLPPPRGLNLLP
 511 YVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILDGYSISSI
 188 ----RARGTN------VTISSLKPDTIYVFQIRARTAAGYGTNSRKFEFE
 397 YLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLS
 ------CSPN-----
 483 -----SYTIL-----
 Gaps
 Query Match
10.2%; Score 611.5; DB 7; Length 983;
Best Local Similarity 24.0%; Pred. No. 2.2e-33;
Matches 208; Conservative 111; Mismatches 259; Indels 287;
PRIOR APPLICATION NUMBER: 60/315,617
PRIOR FILING DATE: 2001-08-29
PRIOR PILING DATE: 2001-07-29
PRIOR PILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/302,358
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-05-29
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-05-02
SOFTWARER OF SEQ ID NOS: 190
SEQ ID NO 59
LENGTH: 983
 369 NIKQCEP-----
 TYPE: PRT
ORGANISM: Homo sapiens
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US-11-203-251A-78

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US-11-203-251A-78

Sequence 78, Application US/11203251A

Publication No. US20060039904A1

GENERAL INFORMATION:

TITLE OF INVENTION: EPH RECEPTOR FC VARIANTS WITH ENHANCED ANTIBODY DEPENDENT

TITLE OF INVENTION: CELL-MEDIATED CYTOTOXICITY ACTIVITY

TITLE OF INVENTION: CELL-MEDIATED CYTOTOXICITY ACTIVITY

TITLE OF TOWNER APPLICATION NUMBER: US/11/203,251A

CURRENT FILING DATE: 2005-08-15

PRIOR FULL DATE: 2004-08-16

PRIOR PRILING DATE: 2004-08-16

PRIOR PRILING DATE: 2004-08-16

NUMBER: OF SEQ ID NOS: 101

SOSTWARE: PatentIn version 3.3
1012 YSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLM 1071
 798 YRKFTSASDVWSYGIVLWEVMSYGERPYWEMSNQDVIKAVDEGYRLPPPMDCPAALYQLM 857
 435
 136 PFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGPIKSKKLLYKPVNHYBAWQHI 495
 554 KSQTTIN----LTWQPIFPSSEDDFYVEVERRSVQKSDQQNIKVPGNLTSVLLNNLHPREQ 610
 487
 671 TIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLEPETAYQVDIFAENNIGSSNPAFSHELV 730
 731 TLPESQAPADIGG--GKMLLIAILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQNV 788
 376 PLPTNEEMTLVKPDGTVLHPKDFNHTDHFSVAIFTIHRILPPDSGVWVCSVNTVAGMVEK
 496 OVTNEIVTLNYLEPRIEYELCVOLVRRGEGGEGHPGPVRRFTTASI--GLPPPRGLNLLP
 389 -LINTIVITOLLAHINYTFEIDAV---NGVSELSSPPROFAAVSITTNQAAPSPVLTIK
 611 YVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSSAVISWTILDGYSISSI
 -----SATIL
 ----RARGTN-------VTISSLKPDT1YVFQIRARTAAGYGTNSRKFEFE
 284 PYG-CSCATGW--KGLQCNEACHPGFY-GPDCKLRCS-C--NNGEMCDRFOGCLCSPGW-
 253 PIGKCSCNAGYEERGFWC-QACRPGFYKALDGNMKCAKCPPHSSTQEDGSMNCRCENNYF
 336 -----QGLQCEREGIPRMTPK------IVDLPDHIEVNSGK---FNPICKASGW
 ------CSbN-----
 Query Match 10.2%; Score 611.5; DB 7; Length 983; Best Local Similarity 24.0%; Pred. No. 2.2e-33; Matches 208; Conservative 111; Mismatches 259; Indels 287; Gaps
 445 KDRTSRNSISLSWQE--PEHPNGIILDYEVKYYEKQEQET------
 1072 RQCWREKPYERPSFAQILVSLNRML 1096
 ORGANISM: Homo sapiens
US-11-203-251A-78
 SEQ ID NO 78
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983 FGLSR---GQEVYVKKTMGRLPVRMMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPY 1039
 1040 CGMTC-AELYEKIPQGYRLEKPINCDDEVYDIMRQCWREKPYERPSFAQIIVSINRMLEE 1098
 867 PGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCMDADFLKRPTFKQIVQLIEKQISE 926
476 IKSKKLLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRR 535
 755 AGMICLIVILAFLIILQLKRANVQRRMAQAFQNVREEPAVQFNSGTLALNRKVKNN---P 811
 863 KDDHRDFAGELEVICKIGHHPNIINLIGACEHRGYLYLAIEYAPHGNLLDFLRKSR---- 918
 687 CSKQEDHAEAALYKNILHSKESSCSDSTNEYMDMKPGVSYVVPTKADKRRSVRIGSYIER 746
 982
 923 DPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIAD
147 DVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHGRITKICD
 536 FTTASIGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIK-VP
 -----TFTDKWED-YPKSENESNI----RYVSELHLTRLKGTE
 387 GGTYTFLVSNSDVNAAIAFNVYVNTKPEILTYDRLVNGMLQCVAAGFPE-----
 655 AVISWTILDG----YSISSITIRYKVQGKNEDQHVDVKIKNAT-----IIQYQLKGLE
 436 PTIDWYPCPGTEQRCSASVLP------VDVQTLNSSGPPFGKLVVQSSIDSSA
 529 AGMMCIIVMILTYKYLQKPMYEVQWKVVBEING-----------NNYVYI
 812 DPTIYPV-LDW----NDIKFQDVIGEGNFGQVLKAR----IKKDGLRMDAAIKRMKEYAS
 595 GNLTSVLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSS
 704 PETAYOVDIFAENNIGSSNPAFS-----HELVTLPESQAPADLGGGKMLLIAILGS
 NS-11-148-770-31

Sequence 31, Application US/11148770

Sequence 31, Application US/11148770

Publication No. US20060019280A1

GENERAL INPORMATION:

APPLICANT: CHEN, LEI L.

TITLE OF INVENTION: MUTATIONS IN KIT CONFER IMATINIB RESISTANCE IN

TITLE OF INVENTION: GASTROINTESTINAL STROMAL TUMORS

FILE REFERENCE: UTXC: 8659US

CURRENT APPLICATION NUMBER: US/11/148,770

FRIOR APPLICATION NUMBER: 60/578,403

PRIOR APPLICATION NUMBER: 60/578,403

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 31

LENGTH: 976
 1099 RKTYVNTTL 1107
 927 STNHIYSNL 935
 ORGANISM: Homo sapiens
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 957 QKQFIHRDLAARNILVGENYVAKIADFGLSRGQE-----VYVKKTMGRLPVRWMAIESLN 1011
 1012 YSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLM 1071
 ::||||||||| : |::|||||| | 339 DMGYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTRG-GKIPIRWTSPEAIA 797
 838 VLKARIKKDGLR-MDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRG 896
 694 PVMIVTEYMENGSLDSFLRKH-----DAQFTVI------QLVGMLRGIASGMKYLS 738
 206 LIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGECICPPGFMGRTCEKACELH----- 258
 259 -----TFGRICKERCSGQEGCKS--YVFCLPDPYGCSCATGWKGLQCNEACHPGFYGP-- 309
 83 ITEKAEATNTGKYTCTNKHGLSNSIYVF-VRDPAKLFLV------DRSLYGKED 129
 LOC--EREGIPRATPKIVDLPDHIEVNSGKFNPICKA-----SGWPLPTNEEMTLV- 386
 -----KPDGTVL------HPKDFNHTDHFSVAIFTIHRILPPDSGVWVC 424
 SVNTVAG-------MVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGP 475
789 REEPAVQFNSGTLALNRKVKNNPDPTIY------PVLDWNDIKFQDVIGEGNFGQ 837
 -----LCSPGWQG 337
 291 YANNTFGSANVTTLEVVDKGF---INIFPM-INTTVFVNDGENVDLI-----334
 897 YLYLAIBYAPHGNILDFIRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLS
 46 LIVR-----VGDBIRLLCT-------DPGFVKWTFEILDETNENKQNEW
 Query Match 10.1%; Score 610; DB 7; Length 972; Best Local Similarity 23.5%; Pred. No. 2.7e-33; Matches 256; Conservative 121; Mismatches 326; Indels 386; Gaps
 RESULT 10

SOLUTION

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PUBlication No. US20060040292A1

CENERAL INFORMATION:

APPLICANT: West, at al.

TITLE OF INTENTION: Tumor Markers and Uses Thereof

FILE REFERENCE: 2002850-0048

CURRENT APPLICATION NUMBER: US/11/177,894

CURRENT FILING DATE: 2005-07-08

NUMBER OF SEQ ID NOS: 29

SOFUTANE: Patentin version 3.2

SOLUTION NOS: 29

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SOLUTION NOS: 29
 , OTHER INFORMATION: KIT amino acid sequence US-11-177-894-17
 1072 RQCWREKPYERPSFAQILVSLNRML 1096
 858 LDCWQKDRNNRPKFEQIVSILDKLI 882
 310 -DCKLRCSCNNGEMCD-RFQGC----
 ORGANISM: Artificial
 338
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 FEATURE:
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1036 GTPYCGMTC-AELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNR 1094
 SVNTVAG------MVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGP 475
 476 IKSKKLLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGFVRR 535
 436 PTIDWYFCPGTEQRCSASVLP------VDVQTLNSSGPPFGKLVVQSSIDSSA 482
 | : : | | : : | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 310 -DCKLRCSCNNGEMCD-RFQGC----LCSPGWQG
 LOC--EREGIPRATPKIVDLPDHIEVNSGKFNPICKA-----SGWPLPTNEEMTLV-
 53 6 FTTASIGLPPPRGLNLLPKSOTTLNLTWOPIFPSSEDDFYVEVERRSVQKSDQQNIK-VP
 | : |::|
|GTYTFLVSNSDVNAA1AFNVYVNTKPE1LTYDRLVNGMLQCVAAGFPE------
 655 AVISWTILDG----YSISSITIRYKVQGKNEDQHVDVKIKNAT-----IIQYQLKGLE
 206 LIVRRCEAQKWGPECNHLCTACMNGVCHEDTGECICPPGFMGRTCEKACELH----
 259 ----TFGRTCKERCSGQEGCKS--YVFCLPDPYGCSCATGWKGLQCNEACHPGFYGP--
 ------KPDGTVL-----HPKDFNHTDHFSVAIFTIHRILPPDSGVWVC
 GNLTSVLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSS
 46 LIVR-----VGDEIRLICT-------DPGFVKWTFEILDETNENKQNEW
 10.1%; Score 608; DB 7; Length 976; 23.4%; Pred. No. 3.7e-33;
 Indels
 Sequence 15, Application US/11177894
Publication No. US20060040292A1
GENERAL INFORMATION:
ITTLE OF INVENTION:
FILE REFERENCE: 2002850-0048
CURRENT APPLICATION NUMBER: US/11/17,894
CURRENT FILING DATE: 2005-07-08
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.2
 Matches 256; Conservative 121; Mismatches 326;
 OTHER INFORMATION: KIT amino acid sequence
 1107
 927 QISESTNHIYSNL 939
 1095 MLEERKTYVNTTL
 ORGANISM: Artificial
 Similarity
 US-11-177-894-15
 ; OTHER INFORM
US-11-177-894-15
 SEQ ID NO 15
LENGTH: 976
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 Query Match
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 KIADFGLSR---GQEVYVKKTMGRLPVRMMAIESLNYSVYTTNSDVWSYGVLLWEIVSLG 1035
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 259 ----TFGRICKERCSGOEGCKS--YVFCLPDPYGCSCATGWKGLQCNEACHPGFYGP-- 309
 310 - DCKLRCSCNNGEMCD-RFQGC----------------------LCSPGWQG 337
 LQC--EREGIPRMTPKIVDLPDHIEVNSGKFNPICKA-----SGWPLPTNEEMTLV- 386
 424
 476 IKSKKLLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRR 535
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 -----VDVQTLNSSGPPFGKLVVQSSIDSSA 482
 ------ 5LLIG 528
 GNLTSVLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSS 654
 82
 | :|| : || : ||
| NDTLVRCPLTDPEVTNYSLKGCQGKPLPKDLRFIPDPKAGIMIKSVKRAYHRLC-----
 291 YANNIFGSANVITILEVVDKGF---INIFPM-INTTVFVNDGENVDLI------
 PETAYQVDIFAENNIGSSNPAFS------HELVTLPESQAPADLGGGKMLLIA
 : ||| |: |:: || FVIVAGMMCIIVMILITYKYLQKPMYEVQWKVVEEING-------NN
 568 YVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDA-AMTVAVKMLK
 SVNTVAG-------MVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGP
 536 FTTASIGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIK-VP
 655 AVISWTILDG----YSISSITIRYKVQGKNEDQHVDVKIKNAT-----IIQYQLKGLE
 EYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSR
 919 VLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVA
 206 LIVRRCEAQKWGPECNHLCTACMNGVCHEDTGECICPPGFMGRTCEKACELH-----
 46 LIVR-----VGDEIRLLCT-------DPGFVKWTFEILDETNENKQNEW
 83 ITEKAEATNIGKYTCINKHGLSNSIYVF-VRDPAKLFLV-------DRSLYGKED
 ------KPDGTVL------KPKDFNHTDHFSVAIFTLHRILPPDSGVWVC
 -----VEYEAF-----VEYEAF-----
 387 GCTYTFLVSNSDVNAAIAFNVYVNTKPEILTYDRLVNGMLQCVAAGFPE------
 ILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQNVREEPAVQFNSGTLALNRKVKNN
 ---PDPTIYPV-LDW----NDIKFQDVIGEGNFGQVLKAR----IKKDGLRMDAAIKRMK
 687 DSFICSKQEDHAEAALYKNLLHSKESSCSDSTNEYMDMKPGVSYVVPTKADKRRSVRIGS
 Gaps
 Query Match 10.1%; Score 608; DB 7; Length 976; Best Local Similarity 23.4%; Pred. No. 3.7e-33; Matches 256; Conservative 121; Mismatches 326; Indels 390;
 PKHNGTVECKAYNDVGKTSAYFNFAFKGNNKEQIHPHTLFT-
 PTIDWYFCPGTEQRCSASVLP----
US-11-148-770-31
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338 LQCERECIPRATPKIVDLPDHIEVNSGKENPICKASGWPLPTHEEWTLVSGWPLPTHEEWTLVSGWPLPTHEEWTLVSGWPLPTHEEWTLV	OY 536 FTTASIGLEPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQONIK-VP 594  Db 354TFTDKWED-YPKSENBSNIRYVSELHLTRLKGTE 386  QY 595 GNLTSVLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSS 654  Db 387 GGTYTFLVSNSDVNAAIAFNVYVNTKPEILTYDRLVNGMLQCVAAGFPE 435  QY 655 AVISWTILDGYSISSITIRYKVQGKNEDOHVDVKIKNATIIQYQLKGLE 703  Db 436 PTIDWYFCPGTEQRCSASVLP	0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0   0.0	RESULT 14 US-11-177-894-18 Sequence 18, Application US/11177894 ; Publication No. US20060040292A1 ; GENERAL INFORMATION: ; APPLICANT: West, et al. ; TITLE OF INVENTION: Tumor Markers and Uses Thereof
104 PETAYQVDIFAENNIGSSNPAFS	DD	1036 GTPYCGMTC-AELYEKIPOGGYRLEKPINCDDEVYDLANGOGWREKPYERPSFAQILVSLAR  167 SSPYGMPUDSKFYKMIKEGFRMLSPEHAPAEMYDLMKTCWDADPLKRPTFKQIUQLIEK  1095 MLEERKTYVNTTL 1107  1	QY         259TFGRICKERCSGQEGCKSYYPCLPDPYGCSCATGWKGLQCNEACHPGFYGP 309           Db         83 ITEKAEATNIGLY

746

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1036 GTPYCGMTC-AELYEKLPQGYRLEKPINCDDEVYDIMRQCWREKPYERPSFAQILVSLNR 1094
 259 ----IPGRICKERCSGQEGCKS--YVPCLPDPYGCSCATGWKGLQCNEACHPGFYGP-- 309
 83 ITEKAEATNTGKYTCTNKHGLSNSIYVF-VRDPAKLFLV------DRSLYGKED 129
 LQC--EREGIPRMTPKIVDLPDHIEVNSGKFNPICKA-----SGWPLPTNEEMTLV- 386
 SVNTVAG------MVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGP 475
 476 IKSKKLLYKPVNHYEAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRR 535
 |: |: |: |: |-----353
 -----KPDGTVL-----HPKDFNHTDHFSVALFTIHRILPPDSGVWVC 424
 687 DSFICSKQEDHAEAALYKNLLHSKESSCSDSTNEYMDMKPGVSYVVPTKADKRRSVRIGS
 919 VLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVA
 979 KIADFGLSR----GQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLG
 807 KICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWSYGIFLWELFSLG
 -----PCSPGMOG
 184 IHCSVDQEGKSVLSEKFI------IKVRPAFKAVPVVSVSKASYLLREGEEFTVTC
 234 TIKDVSSSVYSTWKRENSQTKLQEKYNSWHHGDFNYERQ---ATLTISSARVNDSGVFMC
 46 LIVR-----VGDEIRLLCT------DPGFVKWTFEILDETNENKQNEW
 206 LIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGECICPPGFMGRTCEKACELH----
 Query Match 10.1%; Score 608; DB 7; Length 976; Best Local Similarity 23.4%; Pred. No. 3.7e-33; Matches 256; Conservative 121; Mismatches 326; Indels 390;
 291 YANNIFGSANVITILEVVDKGF---INIFPM-INITVFVNDGENVDLI
 Sequence 20, Application US/11177894
Publication No. US20060040292A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/11/177,894
CURRENT FILING DATE: 2005-07-08
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.2
 310 -DCKLRCSCNNGEMCD-RFQGC------
 ; FEATURE:
- OTHER INFORMATION: KIT amino acid sequence US-111-177-894-20
 ------VEYBAF-----
 1095 MLEERKTYVNTTL 1107
 927 QISESTNHIYSNL 939
 TYPE: PRT
ORGANISM: Artificial
 RESULT 15
US-11-177-894-20
 SEQ ID NO 20
LENGTH: 976
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 259 ----TFGRICKERCSGQEGCKS--YVFCLPDPYGCSCATGWKGLQCNEACHPGFYGP-- 309
 83 ITEKAEATNIGKYTCTNKHGLSNSIYVF-VRDPAKLFLV------DRSLYGKED 129
 234 TIKDVSSSVYSTWKRENSQTKLQEKYNSWHHGDFNYERQ---ATLTISSARVNDSGVFMC 290
 425 SVNTVAG------MVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGDGP 475
 387 GGTYTFLVSNSDVNAAIAFNVYVNTKPEILTYDRLVNGMLQCVAAGFPE------ 435
 751 ILGSAGMTCLTVLLAFLIILQLKRANVQRRMAQAFQNVREEPAVQFNSGTLALNRKVKNN 810
 567
 959 EYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSR 918
 310 - DCKLRCSCNNGEMCD-RFQGC-----------LCSPGWQG 337
 LQC--EREGIPRMTPKIVDLPDHIEVNSGKFNPICKA-----SGWPLPTNEEMTLV- 386
 -------KPDGTVL-----HPKDFNHTDHFSVAIFTIHRILPPDSGVWVC 424
 176 IKSKKLLYKPVNHYBAWQHIQVTNEIVTLNYLEPRTEYELCVQLVRRGEGGEGHPGPVRR 535
 536 FITASIGLPPPRGLNLLPKSQTTLNLTWQPIFPSSEDDFYVEVERRSVQKSDQQNIK-VP 594
 -----TPTDKWED-YPKSENESNI----RYVSELHLTRLKGTE 386
 595 GNLTSVLLNNLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSS 654
 655 AVISWTILDG----YSISSITIRYKVQGKNEDQHVDVKIKNAT-----IIQYQLKGLE 703
 136 PTIDWYPCPGTEQRCSASVLP------VDVQTLNSSGPPFGKLVVQSSIDSSA 482
 PETAYQVDIFAENNIGSSNPAFS------HELVTLPESQAPADLGGGXWLLIA 750
 811 ---PDPTIYPV-LDW----NDIKFODVIGEGNFGQVLKAR----IKKDGLRMDAAIKRMK 858
 206 LIVRRCEAQKWGPECNHLCTACMNNGVCHEDTGECICPPGFMGRTCEKACELH-----
 529 FVIVAGMMCIIVMILTYKYLOKPMYEVOWKVVEBING-------NN
 46 LIVR-----VGDEIRLLCT------DPGFVKWTFEILDETNENKQNEW
 Gaps
 tch 10.1%; Score 608; DB 7; Length 976; al Similarity 23.4%; Pred. No. 3.7e-33; 256; Conservative 121; Mismatches 326; Indels 390;
 291 YANNTFGSANVTTTLEVVDKGF---INIFPM-INTTVFVNDGENVDLI
) OTHER INFORMATION: KIT amino acid sequence US-11-177-894-18
FILE REFERENCE: 2002850-0048
CURRENT APPLICATION NUMBER: US/11/17,894
UNURBER FILING DATE: 2005-07-08
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.2
 TYPE: PRT
ORGANISM: Artificial
 SEQ ID NO 18
LENGTH: 976
 704
 Query Match
Best Local S
 387
 354
 FEATURE:
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Gaps

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536 FTTASIGLPPPRGLNLLPKSGTTLALTWQPIPPSSEDDFYVEVERRSYQKSDQQNIK-VP 594	595 GNLTSVLLANLHPREQYVVRARVNTKAQGEWSEDLTAWTLSDILPPQPENIKISNITHSS 654	655 AVISWTILDGYSISSITIRYKVQGKNEDQHVDVKIKNATIIQYQLKGLE 703	704 PETAYQVDIFABNNIGSSNPAFSHELVILPESQAFADLGGGGWLLIA 750	483 PKHNGTVECKÅYNDVGKTSAYFNPAPKGNNKEQIHPHTLFTPLLIG 528	751 ILGSAGMTCLTVILAFLIILQLKRANVQRRMAQAFQNVREEPAVQFNSGTLALNRKVKNN 810           :   ::           ::         :: :         ::           ::           ::	811PDPITYPV-LDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMK 858	568 YVYIDPTQLPYDHKWEFPRNRLSFGKTLGAGAFGKVVEATAYGLIKSDA-AMTVAVKMLK 626	859 EYASKDDHRDFAGELEVLCKLGHPPNIINLLGACEHRGYLYLAIBYAPHGNLLDFLRKSR 918	627 PSAHLTEREALMSELKVLSYLGNHMNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKR 686	916 918	687 DSFICSKQEDHAEAALYKNLLHSKESSCSDSTNEYMDMKPGVSYVVPTKADKRRSVRIGS 746	919 VLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKOFIHRDLAARNILVGENYVA 978	47 YIBRDVTPAIMEDDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILLTHGRIT 806	979 KIADFGLSRGQEVYVKKIMGRLPVR#MAIESLNYSVYTINSDV#SYGVLMEIVSLG 1035	07 KICDFGLARDIKNDSNYVVKGNARLPVKWMAPESIFNCVYTFESDVWSYGIFLWELFSLG 866	1036 GTPYCGWTC-AELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNR 1094	67 SSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMYDIMKTCWDADPLKRPTFKQIVQLIEK 926	1095 MLEERKTYVNITL 1107	927 QISESTWHIYSNL 939	
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